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OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 23:21:40 ; Search time 312 Seconds  
(without alignments)  
3483.830 Million cell updates/sec

Title: US-10-824-981-1  
Perfect score: 1343  
Sequence: 1 ctcgaggatctcgccggc.....atacccttaaatgaggtacc 1343

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6038814 seqs, 404674181 residues

Total number of hits satisfying chosen parameters: 12077628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330.8	99.1	2755	8	US-11-000-688-73
2	205.6	15.3	269	8	Sequence 73, Appl
3	204.2	15.2	472	8	Sequence 72, Appl
4	204.2	15.2	472	8	Sequence 2285, Ap
5	53.4	4.0	387	8	Sequence 5927, Ap
6	40.8	3.0	598	7	Sequence 71, Appl
7	40.8	3.0	598	7	Sequence 21506, A
8	39.6	2.9	1236	7	Sequence 21506, A
9	39.6	2.9	1236	7	Sequence 59374, A
10	39.4	2.9	1542	7	Sequence 59374, A
11	39.4	2.9	1542	7	Sequence 51728, A
12	39.4	2.9	1659	7	Sequence 51728, A
13	39.4	2.9	4419	7	Sequence 47, Appl
14	39.4	2.9	4419	7	Sequence 25730, A
15	38.8	2.9	191331	8	Sequence 25730, A
16	38.6	2.9	1519	7	Sequence 20, Appl
17	38.6	2.9	1519	7	Sequence 46824, A
18	38.6	2.9	1959	8	Sequence 46824, A
19	38.4	2.9	172649	8	Sequence 3, Appl
20	37.8	2.8	21142	7	Sequence 36, Appl
21	37.6	2.8	3001	8	Sequence 13380, A
22	37.4	2.8	5562	7	Sequence 178, App
					Sequence 63, Appl

23	37	2.8	83528	7	US-10-995-561-13343	Sequence 13343, A
24	37	2.8	1080000	7	US-10-928-446A-1	Sequence 1, Appl
25	37	2.8	1080000	7	US-10-928-446A-181	Sequence 181, App
26	37	2.8	1080000	7	US-10-928-446A-183	Sequence 183, App
27	37	2.8	1080000	7	US-10-928-446A-185	Sequence 185, App
28	37	2.8	1080000	7	US-10-928-446A-187	Sequence 187, App
29	37	2.8	1080000	7	US-10-928-446A-189	Sequence 189, App
30	37	2.8	1080000	7	US-10-928-446A-191	Sequence 191, App
31	37	2.8	1080000	7	US-10-928-446A-193	Sequence 193, App
32	37	2.8	1080000	7	US-10-928-446A-195	Sequence 195, App
33	37	2.8	1080000	7	US-10-928-446A-197	Sequence 197, App
34	37	2.8	1080000	7	US-10-928-446A-199	Sequence 199, App
35	37	2.8	1080000	7	US-10-928-446A-201	Sequence 201, App
36	36.8	2.7	600	7	US-10-750-185-756	Sequence 756, App
37	36.8	2.7	600	7	US-10-750-185-756	Sequence 756, App
38	36.8	2.7	918	7	US-10-750-185-38838	Sequence 38838, A
39	36.8	2.7	918	7	US-10-750-185-38838	Sequence 38838, A
40	36.4	2.7	764	7	US-10-750-185-59751	Sequence 59751, A
41	36.4	2.7	764	7	US-10-750-185-59751	Sequence 59751, A
42	36.4	2.7	1685	7	US-10-750-185-29078	Sequence 29078, A
43	36.4	2.7	1685	7	US-10-750-185-29078	Sequence 29078, A
44	36.4	2.7	1994	7	US-10-750-185-26833	Sequence 26833, A
45	36.4	2.7	1994	7	US-10-750-185-26833	Sequence 26833, A

ALIGNMENTS

RESULT 1

US-11-000-688-73  
; Sequence 73, Application US/11000688  
; Publication No. US20050287544A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTUCCI, Francois  
; APPLICANT: HOULGATTE, Remi  
; APPLICANT: BIRNBAUM, Daniel  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS  
; FILE REFERENCE: 1423-R-03  
; CURRENT APPLICATION NUMBER: US/11/000,688  
; PRIOR FILING DATE: 2004-12-01  
; PRIOR APPLICATION NUMBER: US 60/525,987  
; PRIOR FILING DATE: 2003-12-01  
; NUMBER OF SEQ ID NOS: 1596  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 73  
; LENGTH: 2755  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial sequences:primer  
; NAME/KEY: misc feature  
; LOCATION: (1)..(2755)  
; OTHER INFORMATION: Interferon (alpha, beta and omega) receptor  
; OTHER INFORMATION: 1(IFNARI) gene.  
US-11-000-688-73

Query Match 99.1%; Score 1330.8; DB 8; Length 2755;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CTGCAGGGATCTGCGGGGCTCCAGATGATGGTCTCTCTGGGCGGACGACCTAG	60
Db	53	CTGTGGGATCTGCGGGGCTCCAGATGATGGTCTCTCTGGGCGGACGACCTAG	112
Qy	61	TGCTGTGCGCGTGGGCGCATGGTGTGTCCGAGCGCGAGGTGGAAAAATCTAAAT	120
Db	113	TGCTGTGCGCGTGGGCGCATGGTGTGTCCGAGCGCGAGGTGGAAAAATCTAAAT	172
Qy	121	CTCTCAAAAGTAGAGTCCACATCATAGTACACTTTATCTGAGGTGGACAGGA	180
Db	173	CTCTCAAAAGTAGAGTCCACATCATAGTACACTTTATCTGAGGTGGACAGGA	232

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QY 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAACAAAAAATCGGATGGATA 240
Db 233 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAACAAAAAATCGGATGGATA 292
QY 241 ATTGGATAAAATGCTCTGGGTGTCAGATATTAAGTACCAATGCAATTTCTTTCAC 300
Db 293 ATTGGATAAAATGCTCTGGGTGTCAGATATTAAGTACCAATGCAATTTCTTTCAC 352
QY 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGGCTTAAGAGCAGAAAAAGAAAAACACTT 360
Db 353 TCAAGCTGAATGTTTATGAAGAAATTAATTTGGCTTAAGAGCAGAAAAAGAAAAACACTT 412
QY 361 CTTTCATGATGATGAGTTGACTCAATTTACACATTTCCAAAGCTCAGATTTGGTCTCCAG 420
Db 413 CTTTCATGATGAGTTGACTCAATTTACACATTTCCAAAGCTCAGATTTGGTCTCCAG 472
QY 421 AAGTACATTTAGAGCTGAAGATAAGGCATAGTGATACACATCTCTCCCTGGAAACAAAAG 480
Db 473 AAGTACATTTAGAGCTGAAGATAAGGCATAGTGATACACATCTCTCCCTGGAAACAAAAG 532
QY 481 ATAGTGTATGTCGGCTTTTCGATGTTTAAGCTTTACATATAGCTTACATATAGCTTACAT 540
Db 533 ATAGTGTATGTCGGCTTTTCGATGTTTAAGCTTTACATATAGCTTACATATAGCTTACAT 592
QY 541 ACTCTTCAGGTGTAGAGAAAGGATGAAATATTTATCCAGACATATAAAATTTATAAAC 600
Db 593 ACTCTTCAGGTGTAGAGAAAGGATGAAATATTTATCCAGACATATAAAATTTATAAAC 652
QY 601 TCTCACGAGACTACTTATTTGCTTAAAGTTAAAGCAGCACTACTTACGTATGGAATA 660
Db 653 TCTCACGAGACTACTTATTTGCTTAAAGTTAAAGCAGCACTACTTACGTATGGAATA 712
QY 720 TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAAGTTGAAATGAATGAATCACTCCAC 720
Db 713 TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAAGTTGAAATGAATGAATCACTCCAC 772
QY 721 CAGAAATATPAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780
Db 773 CAGAAATATPAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 832
QY 781 ATGCAACATGACCTTTCAAGTTTCAGTGGTCCAGCGCTTTTAAAGGAATCTCTGGAA 840
Db 833 ATGCAACATGACCTTTCAAGTTTCAGTGGTCCAGCGCTTTTAAAGGAATCTCTGGAA 892
QY 841 ACCATTTGTATAATGGAACCAATACCTGACTGTGAAATGTCAAACTACCCAGGTG 900
Db 893 ACCATTTGTATAATGGAACCAATACCTGACTGTGAAATGTCAAACTACCCAGGTG 952
QY 901 TCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAGCATCTGATG 960
Db 953 TCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAGCATCTGATG 1012
QY 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAGCTTTCC 1020
Db 1013 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAGCTTTCC 1072
QY 1021 TACTTCTCCAGTCTTTAAATAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1080
Db 1073 TACTTCTCCAGTCTTTAAATAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1132
QY 1081 CTCAAAAACAGTCTGAAACACGCGCTGTGATCCAGGATTTACCATGATTTATGAATTA 1140
Db 1133 CTCAAAAACAGTCTGAAACACGCGCTGTGATCCAGGATTTACCATGATTTATGAATTA 1192
QY 1141 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTTATCGAGAAAAAAATCTGATGTTA 1200
Db 1193 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTTATCGAGAAAAAAATCTGATGTTA 1252
QY 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTTGAAAGCCAGAGCACACCATG 1260
Db 1253 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTTGAAAGCCAGAGCACACCATG 1312
QY 1261 ATGAAAAGCTGAATAAAGCAGTGTGTTTATAGTCACGCTGTATGTGAGAAAAAACCAG 1320
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## RESULT 2

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US-11-000-688-72
; Sequence 72, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; PRIOR FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences: primer
; NAME/KEY: misc feature
; LOCATION: (1)-(269)
; OTHER INFORMATION: 5' terminal sequence from clone
; OTHER INFORMATION: image:121265, interferon (alpha, beta and omega)
; OTHER INFORMATION: receptor 1 (IFNARI) gene.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (254)-(254)
; OTHER INFORMATION: n is a, c, g, or t
US-11-000-688-72
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Query Match 15.3%; Score 205.6; DB 8; Length 269;  
Best Local Similarity 95.5%; Pred. No. 3.3e-46;

Matches 233; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

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QY 611 GACTACTTATTGCTTAAAGTTAAAGCAGCAGCTACTTACGTCATGGAATAATTCGTGCTA 670
Db 1 GACTACTTATTGCTTAAAGTTAAAGCAGCAGCTACTTACGTCATGGAATAATTCGTGCTA 60
QY 671 TAGTCCAGTACATTTGATTAAGACCAAGTTCGAAATGAATGAATCACTCCACGAAATAT 730
Db 61 TAGTCCAGTACATTTGATTAAGACCAAGTTCGAAATGAATGAATCACTCCACGAAATAT 120
QY 731 AGAAGTCAGTCTCCAAAAATCAGAACTATCTTCTTAAATGGGATTATACATATGCAAAACAT 790
Db 121 AGAAGTCAGTCTCCAAAAATCAGAACTATCTTCTTAAATGGGATTATACATATGCAAAACAT 180
QY 791 GACCTTTT-CAAGTTCAGT-GGCTCCACGCTTTTAAAAAGGAATCCTCGAAACCAATTTG 848
Db 181 GACCTTTTCAAGTTCAGTGGGCTCCACGCTTTTAAAAAGGAATCCTCGGGAACCAATTT 240
QY 849 TATA 852
Db 241 GTTA 244
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## RESULT 3

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US-11-128-061-2285
; Sequence 2285, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
```

APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Hann, Louane E.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION  
FILE REFERENCE: 01997.027701  
CURRENT APPLICATION NUMBER: US/11/128,061  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 2285  
LENGTH: 472  
TYPE: DNA  
ORGANISM: Cricetulus griseus  
US-11-128-061-2285

Query Match 15.2%; Score 204.2; DB 8; Length 472;  
Best Local Similarity 64.9%; Pred. No. 1.1e-45;  
Matches 302; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

Qy 460 ACATCTCTCTCGGAACAAAAGATAGTGTATGTGGGCTTTGGATGGTTTAAAGCTTTTACAT 519  
Db 7 ACATCTCTCTATCCCGGACAAAGTGGGAGAGATGGTCAAGCGATATTCTTCGCTTCGAGT 66

Qy 520 ATAGCTTACTTATCTGGAAGAACTCTTCAGGTGTAGAGAGAGATTTGAAATATTATT 579  
Db 67 ACAGGGTAGTAATCTGCGAGAAGTCTTCCAATGAGACACAGAGATTACCAACCACTTATT 126

Qy 580 CCAGACATAAAATTTATAAATCTCCAGAGACTTACTTATGTCTAAAAGTTAAAGCAG 639  
Db 127 ATACAGAAAGATTTCAAACTGTTCAGAGACTTACTTGTCTAAAAGTTAAAGCAA 186

Qy 640 CACTACTTACGTATGGAATTTGGTGTCTATAGTCCAGTACATTTGTATAAAGACCAACAG 699  
Db 187 TACATTCGTCCTCGGAAACACAGCAATTTATGTGCGATGCAATGTATTAACCACTATG 246

Qy 700 TTGAAATGAAGTACTCTCCAGAGAAATATAGAAAGTCAAGTGTCCAAAATCAGAACTATG 759  
Db 187 TACATTCGTCCTCGGAAACACAGCAATTTATGTGCGATGCAATGTATTAACCACTATG 246

Qy 760 TTCTTAAATGGATATACATATAGAAAGTCAAGTGTCCAAAATCAGAACTATG 819  
Db 247 AGGCCATCAAGTCCAGTCCGGAACACATATAAGTGGATGCCCGTGGTGGAGAGCTATG 306

Qy 820 TTTTAAAAGGAACTCTCGGAACCAATTTGTATTAATGGAACCAATACCTGACTGTGAAA 879  
Db 367 ATTTTAAAGTATCTCTGGAAGCTCTTCAAATGAATGGAACCAATACCTGACTGTGAAA 426

Qy 880 ATGTCAAAATACCGAGTGTCTTTCTCAAAACGTTTTCCTCAAA 924  
Db 427 ATGTCAAAATACCGAGTGTCTTTCTTAAACCAACCAATCCACA 471

RESULT 4  
US-11-128-061-5927  
Sequence 5927, Application US/11128061  
Publication No. US20060003958A1  
GENERAL INFORMATION:  
APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Hann, Louane E.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS

TITLE OF INVENTION: TO MONITOR GENE EXPRESSION  
FILE REFERENCE: 01997.027701  
CURRENT APPLICATION NUMBER: US/11/128,061  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5927  
LENGTH: 472  
TYPE: DNA  
ORGANISM: Cricetulus griseus  
US-11-128-061-5927

Query Match 15.2%; Score 204.2; DB 8; Length 472;  
Best Local Similarity 64.9%; Pred. No. 1.1e-45;  
Matches 302; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

Qy 460 ACATCTCTCTCGGAACAAAAGATAGTGTATGTGGGCTTTGGATGGTTTAAAGCTTTTACAT 519  
Db 7 ACATCTCTCTATCCCGGACAAAGTGGGAGAGATGGTCAAGCGATATTCTTCGCTTCGAGT 66

Qy 520 ATAGCTTACTTATCTGGAAGAACTCTTCAGGTGTAGAGAGAGATTTGAAATATTATT 579  
Db 67 ACAGGGTAGTAATCTGCGAGAAGTCTTCCAATGAGACACAGAGATTACCAACCACTTATT 126

Qy 580 CCAGACATAAAATTTATAAATCTCCAGAGACTTACTTATGTCTAAAAGTTAAAGCAG 639  
Db 127 ATACAGAAAGATTTCAAACTGTTCAGAGACTTACTTGTCTAAAAGTTAAAGCAA 186

Qy 640 CACTACTTACGTATGGAATTTGGTGTCTATAGTCCAGTACATTTGTATAAAGACCAACAG 699  
Db 187 TACATTCGTCCTCGGAAACACAGCAATTTATGTGCGATGCAATGTATTAACCACTATG 246

Qy 700 TTGAAATGAAGTACTCTCCAGAGAAATATAGAAAGTCAAGTGTCCAAAATCAGAACTATG 759  
Db 247 AGGCCATCAAGTCCAGTCCGGAACACATATAAGTGGATGCCCGTGGTGGAGAGCTATG 306

Qy 760 TTCTTAAATGGATATACATATAGAAAGTCAAGTGTCCAAAATCAGAACTATG 819  
Db 307 TTCTGAAATGGAGTGTGCGTCTACAGACGTGAGCTTCAGAACGCGAGTGGCTCCCTGGCT 366

Qy 820 TTTTAAAAGGAACTCTCGGAACCAATTTGTATTAATGGAACCAATACCTGACTGTGAAA 879  
Db 367 ATTTTAAAGTATCTCTGGAAGCTCTTCAAATGAATGGAACCAATACCTGACTGTGAAA 426

Qy 880 ATGTCAAAATACCGAGTGTCTTTCTCAAAACGTTTTCCTCAAA 924  
Db 427 ATGTCAAAATACCGAGTGTCTTTCTTAAACCAACCAATCCACA 471

RESULT 5  
US-11-000-688-71/c  
Sequence 71, Application US/11000688  
Publication No. US2005028754A1  
GENERAL INFORMATION:  
APPLICANT: BERTUCCI, Francois  
APPLICANT: HOULGATTE, Remi  
APPLICANT: BIRNBAUM, Daniel  
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS  
FILE REFERENCE: 1423-R-03  
CURRENT APPLICATION NUMBER: US/11/000,688  
CURRENT FILING DATE: 2004-12-01  
PRIOR APPLICATION NUMBER: US 60/525,987  
PRIOR FILING DATE: 2003-12-01  
NUMBER OF SEQ ID NOS: 1596  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 71  
LENGTH: 387  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial sequences: primer

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(387)
; OTHER INFORMATION: 3' terminal sequence from clone
; OTHER INFORMATION: image:121265, interferon (alpha, beta and omega)
; OTHER INFORMATION: receptor 1 (IFNAR1) gene.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (291)..(292)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (309)..(309)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (312)..(312)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (323)..(323)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (331)..(331)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (346)..(346)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (364)..(364)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (381)..(381)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-000-688-71
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Query Match 4.0%; Score 53.4; DB 8; Length 387;
Best Local Similarity 75.0%; Pred. No. 9e-05;
Matches 90; Conservative 0; Mismatches 26; Indels 4; Gaps 2;

QY 1078 GTGCTCAAAACAGCTCGGAAACACGCC---TGATGATCCAGGATTAT-CCACTGATTTAT 1133
Db 325 GCNCCAAACAGCNCNGGAAACACGCCCTGTGNNCCCCAGGATTATCCCACTGATTTAT 266

QY 1134 GAAATATTTTTTGGGAAACACTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAAACT 1193
Db 265 GAAATATTTTTTGGGAAACACTTCAAATGCTGAGGTAAGAAAGACTGTATAGTATAATT 206
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RESULT 6
US-10-750-185-21506/c
; Sequence 21506, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
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; SEQ ID NO 21506
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Bovine MMBT10464
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(47)
; OTHER INFORMATION: n is any nucleotide
; US-10-750-185-21506
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Query Match 3.0%; Score 40.8; DB 7; Length 598;
Best Local Similarity 48.3%; Pred. No. 0.3;
Matches 111; Conservative 1; Mismatches 118; Indels 0; Gaps 0;

QY 436 CTGAAGATAAGCAATAGTGATACACATCTCTCTGGAAACAAAGATAGTGTATGTGGG 495
Db 505 CTAAGAAAGATAAATATTAGTATACAAAGCTAAATATTTTCGTACAAATATTTTATCCCT 446
QY 496 CTTTGATGGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAAAACTCTTCAGAGTGTAG 555
Db 445 TCTAGGAGATATTCAGAGAGTTATTTTCTAGTTTCTTAGAAGATTTTCATTGGTCTAG 386
QY 556 AAGAAAGGATTGAAATATTTATTCAGACATAAAATTTATAAATCTCTCACAGAGACTA 615
Db 385 TATAATTTTACCACATGCCCTATTTAAAAACAAATAAATTAGAAATTTTAAAAACAGTATT 326
QY 616 CTTATTGCTCTAAAGTTAAAGCAGCACTACTTACGTCATCGGAAAAATGGT 665
Db 325 ATATTGTATACCTCTGTAATGCTGTRCTACTTTTCTCCTTAATTGTGGT 276
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RESULT 7
US-10-750-623-21506/c
; Sequence 21506, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 21506
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Bovine MMBT10464
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(47)
; OTHER INFORMATION: n is any nucleotide
; US-10-750-623-21506
```

```
Query Match 3.0%; Score 40.8; DB 7; Length 598;
Best Local Similarity 48.3%; Pred. No. 0.3;
Matches 111; Conservative 1; Mismatches 118; Indels 0; Gaps 0;

QY 436 CTGAAGATAAGCAATAGTGATACACATCTCTCTGGAAACAAAGATAGTGTATGTGGG 495
Db 505 CTAAGAAAGATAAATATTAGTATACAAAGCTAAATATTTTCGTACAAATATTTTATCCCT 446
QY 496 CTTTGATGGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAAAACTCTTCAGAGTGTAG 555
Db 445 TCTAGGAGATATTCAGAGAGTTATTTTCTCCTAGTTTCTTAGAAGAAATTCATTGGTCTAG 386
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Db 569 TAAATTTGTTCAAGAGGTTAATAAAGACCTTTAGGAATAATTTGCCCTTCTGTTTATAT 628  
Qy 518 ATATAGCTTACTTATCTGGAATAACTCTTCAGGTGTAGAGAAAGGATTTGAAATATTTA 577  
Db 629 ATATACAAATATAAATTTTAAAGTTTCTATTTTGTGTAAATTTACATTTTAAATATACATAA 688  
Qy 578 TTCCAGACATATAAATTTTATAAATCTCTCACCAGACACTTATTTGTCTTAAAGTTAAAGC 637  
Db 689 TCCCTAAATTAATAATAATAATATGACATTAATCATGCAAGTTTAAATAGTCAATGT 748  
Qy 638 AGCACTACTTACGTCATGGAATAAT 662  
Db 749 TGATACACTTCCATTTTAAATAAAT 773

## RESULT 11

US-10-750-623-51728  
; Sequence 51728, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 51728  
; LENGTH: 1542  
; TYPE: DNA  
; ORGANISM: Bovine 19866880461197  
US-10-750-623-51728

Query Match 2.9%; Score 39.4; DB 7; Length 1542;  
Best Local Similarity 43.9%; Pred. No. 1.2;  
Matches 169; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

Qy 278 TACCAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTAT 337  
Db 389 TATAAATCTACTCTGCTTTTATCAATATAAACCATTGAGGAATTTATCTTGGAAA 448  
Qy 338 AGAGCAGAAAAGAAACACTTCTTCATCGGTATGAGGTTGACTCAATTTACACCATTTG 397  
Db 449 AATAGTACAAATGTTTGTGATTTTATTTATTAAGATTAATTCACATTAATCTGCAA 508  
Qy 398 CAAGCTCAGATTGGTCTCCAGAGTACATTTTAGAGCTGAAGATAAGCAATAGTAT 457  
Db 509 GTATTAATTTTACTTTTAATAGGAAACTAATATGATTTATGTTCTTCCCTTCAAGGGTT 568  
Qy 458 ACACATCTCTCTGGAACAAAGATGTTATGTGGCTTTGGATGGTTTAAAGCTTTAC 517  
Db 569 TAATTTGTTCAAGAGGTTAATAAAGACCTTTAGGAATAATTTGCCCTTCTGTTTATAT 628  
Qy 518 ATATAGCTTACTTATCTGGAATAACTCTTCAGGTGTAGAGAAAGGATTTGAAATATTTA 577  
Db 629 ATATACAAATATAAATTTTAAAGTTTCTATTTTGTGTAATTAATTTTAAATATACATA 688  
Qy 578 TTCCAGACATAAATTTTAAACTCTCACAGAGACTCTTATTTGCTTAAAGTTAAAGC 637  
Db 689 TCCCTAAAATTAATAATAATAATATGACATTAATCAATGCAAGTTTAAATAGTCAATGT 748  
Qy 638 AGCACTACTTACGTCATGGAATAAT 662  
Db 749 TGATACACTTCCATTTTAAATAAAT 773

RESULT 12  
US-10-636-716-47  
; Sequence 47, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24CI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1659 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...1659  
; OTHER INFORMATION:  
US-10-636-716-47

Query Match 2.9%; Score 39.4; DB 7; Length 1659;  
Best Local Similarity 49.8%; Pred. No. 1.3;  
Matches 128; Conservative 0; Mismatches 126; Indels 3; Gaps 1;

Qy 198 AATGTGACCTTTTTCATTTCGATTATCAAAAACTGGGATCGAATATTTGGATAAAATTTGCT 257  
Db 196 AAGGTTACTTACTGTGCGAGTATTTTATTTATGGCAGAGAAGTGGCTGAATAAGTCA 255  
Qy 258 GGGTGTGCAATATTACTAGTACCAAACTTTTCTTCACTCAAGCTGAATGTTAT 317  
Db 256 GAGTGTGCAATATCAATCGAACCTATTGTGATCTTCTGCTGAGACTTCTGATATGAG 315  
Qy 318 GAAGAATTAATTTGGTATTAAGACGAAAAAACAACCTTCTTC----ATGGTATGAG 374

Db 316 CATCAGTATTATGCCAAGTTTAAGCCATTGGGGACGAAAGTGTTCAGAGTGGGCTGAG 375  
Qy 375 GTTGACTCAITTCACCAATTCGCAAGAGCTCAGATTGGTCTCCAGAGAGTACATTTAGAA 434  
Db 376 AGTGGCGGTTTTATCTCTTTCTAGAGACGAGATTGGCCGCGGAGGTGGCGCTGACT 435  
Qy 435 GCTGAAGATAAGGCAAT 451  
Db 436 ACGGATGGAAGTCAAT 452

## RESULT 13

US-10-750-185-25730/c

; Sequence 25730, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; PRIOR FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25730

; LENGTH: 4419

; TYPE: DNA

; ORGANISM: Bovine 19866881150821

US-10-750-185-25730

Query Match 2.9%; Score 39.4; DB 7; Length 4419;  
Best Local Similarity 45.2%; Pred. No. 2.2;  
Matches 145; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 572 TATTTATCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGCTTAAAGT 631  
Db 733 TAATTAGAAAATACTAAATATACAATCTAGTTCTTTTCATTTCTTTCTGGATAAATAG 674  
Qy 632 TAAAGCAGCACTACTTACGTCATCGAAAATTTGGTGTCTATAGTCCAGTACATTTGTATATA 691  
Db 673 TAGAAGGACATTTTAAAGTAAGATGAATTTGATGTTCTTAAGCATATTAATTTAGAAAA 614  
Qy 692 GACCACAGTTGAAAATGAATGAACTACCTCCACGAGAAAATATAGAAGTCAAGTCCAAAATCA 751  
Db 613 GACCATTAACAAGACAGAAATTTATTTTCTTAAACATTTTAAATCACTGGATAATATCC 554  
Qy 752 GAACATGTTCTTAAATGGGATTATACATATGCAAAACATGACCTTCAAGTTTCAGTGGCT 811  
Db 553 TATTTGTTTCATATTATGTTTATGGGAAAATATGATCTTATTTTCTAGTTTTGATGCT 494  
Qy 812 CCAGCGCTTTTAAAGGAAATCCTCGAAACCAATTTGTATATAATGGAACAAATACCTGA 871  
Db 493 AGAGTCTTTTTTAAATCCAAATAGCATATATTTAATATATGCAATTTTGAAAAGTTAC 434  
Qy 872 CTGTGAAAATGTCAAAACCTAC 892  
Db 433 CTTTTCAAAATCATAACTAC 413

## RESULT 14

US-10-750-623-25730/c

; Sequence 25730, Application US/10750623

; Publication No. US20050287531A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25730  
; LENGTH: 4419  
; TYPE: DNA  
; ORGANISM: Bovine 19866881150821  
US-10-750-623-25730

Query Match 2.9%; Score 39.4; DB 7; Length 4419;  
Best Local Similarity 45.2%; Pred. No. 2.2;  
Matches 145; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 572 TATTTATCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGCTTAAAGT 631  
Db 733 TAATTAGAAAATACTAAATATACAATCTAGTTCTTTTCATTTCTTTCTGGATAAATAG 674  
Qy 632 TAAAGCAGCACTACTTACGTCATCGAAAATTTGGTGTCTATAGTCCAGTACATTTGTATATA 691  
Db 673 TAGAAGGACATTTTAAAGTAAGATGAATTTGATGTTCTTAAGCATATTAATTTAGAAAA 614  
Qy 692 GACCACAGTTGAAAATGAATGAACTACCTCCACGAGAAAATATAGAAGTCAAGTCCAAAATCA 751  
Db 613 GACCATTAACAAGACAGAAATTTATTTTCTTAAACATTTTAAATCACTGGATAATATCC 554  
Qy 752 GAACATGTTCTTAAATGGGATTATACATATGCAAAACATGACCTTCAAGTTTCAGTGGCT 811  
Db 553 TATTTGTTTCATATTATGTTTATGGGAAAATATGATCTTATTTTCTAGTTTTGATGCT 494  
Qy 812 CCAGCGCTTTTAAAGGAAATCCTCGAAACCAATTTGTATATAATGGAACAAATACCTGA 871  
Db 493 AGAGTCTTTTTTAAATCCAAATAGCATATATTTAATATATGCAATTTTGAAAAGTTAC 434  
Qy 872 CTGTGAAAATGTCAAAACCTAC 892  
Db 433 CTTTTCAAAATCATAACTAC 413

## RESULT 15

US-11-112-908-20

; Sequence 20, Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Davis, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 20

; LENGTH: 191331

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-20

Query Match		2.9%	Score 38.8;	DB 8;	Length 191331;
Best Local Similarity		51.1%	Pred. No. 26;		
Matches	91;	Conservative	0;	Mismatches	87;
				Indels	0;
				Gaps	0;
Qy	564	ATTGAAATATTTATTCGAGACATATAAAATTTATAAACTCTCACGAGAGACTACTTATTGT	623		
Db	110325	AATGAAAAAATTTACTTTCTGACCTGACATTCACATCTTTCACTTGAACAAAAACATCTG	110384		
Qy	624	CTAAAGTTAAAGCAGCAGCACTACTTACGTCATGGAAAATTTGGTCTCTATAGTCAGTACAT	683		
Db	110385	ATTTAAGTTCTAGATCTGCCACTTACATTACTGAGAAAGTCATTGAAATGGCTCAGAACCA	110444		
Qy	684	TGTATAAGACCAAGTTGAAAATGAACTACCTCCACGAGAAAATATAGAAGTCAGTG	741		
Db	110445	TCTGTGAAGTGGGACATCATATATACCACCTTGTTAAGTCATTGTGAAAAATATGAG	110502		

Search completed: January 18, 2006, 02:12:44  
Job time : 315 secs



; TYPE: nucleic acid									
; STRANDEDNESS: double									
; TOPOLOGY: linear									
; MOLECULE TYPE: DNA (genomic)									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: 27..1334									
US-09-240-675-1									
Query Match 100.0%; Score 1343; DB 3; Length 1343;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	CTGAGGAGATCTGGCGGGCTCCAGATGATGTGCTCTCTCGGGCGGCGACGCCCTAG	60						
DB	1	CTGAGGAGATCTGGCGGGCTCCAGATGATGTGCTCTCTCGGGCGGCGACGCCCTAG	60						
QY	61	TGCTGTGCGCGTGGGCCCATGGGTGTGTCGCGAGCGCGAGGTGGAAAAATCTAAAT	120						
DB	61	TGCTGTGCGCGTGGGCCCATGGGTGTGTCGCGAGCGCGAGGTGGAAAAATCTAAAT	120						
QY	121	CTCTCAAAAGTAGAGGTGCGATCATAGATGACAACTTTTCAATTCGAATTATCAAAAACTGGGATGGATA	180						
DB	121	CTCTCAAAAGTAGAGGTGCGATCATAGATGACAACTTTTCAATTCGAATTATCAAAAACTGGGATGGATA	180						
QY	181	GCGATGAGTCTGTCGGGAATGTGACTTTTCAATTCGAATTATCAAAAACTGGGATGGATA	240						
DB	181	GCGATGAGTCTGTCGGGAATGTGACTTTTCAATTCGAATTATCAAAAACTGGGATGGATA	240						
QY	241	ATTGGATAAAATGTCTGGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTTCAC	300						
DB	241	ATTGGATAAAATGTCTGGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTTCAC	300						
QY	301	TCAGCTGAATGTTTATGAAGAAATTAATTTGGTATAGAGCAGAGAAAGAAACACTT	360						
DB	301	TCAGCTGAATGTTTATGAAGAAATTAATTTGGTATAGAGCAGAGAAAGAAACACTT	360						
QY	361	CTTCATGGTATGAGTGTGACTTTACACCATTTCCAAAGCTCAGATTGGTCTCCAG	420						
DB	361	CTTCATGGTATGAGTGTGACTTTACACCATTTCCAAAGCTCAGATTGGTCTCCAG	420						
QY	421	AAGTACATTTAAGCTGGAAGATAAGGCAATAGTGATACATCTCTCTGGAAACAAAG	480						
DB	421	AAGTACATTTAAGAGCTGGAAGATAAGGCAATAGTGATACATCTCTCTGGAAACAAAG	480						
QY	481	ATAGTGTATGTGGCTTTCCGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAA	540						
DB	481	ATAGTGTATGTGGCTTTCCGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAA	540						
QY	541	ACTCTTCAGGTGTAGAAAGAGATTGAAAATATTTATTCAGACATATAAATTTATAAC	600						
DB	541	ACTCTTCAGGTGTAGAAAGAGATTGAAAATATTTATTCAGACATATAAATTTATAAC	600						
QY	601	TCTCACCAGAGACTTACTTATGTCTAAAGTTAAGCAGCACTACTTTACGTCTAGGAAA	660						
DB	601	TCTCACCAGAGACTTACTTATGTCTAAAGTTAAGCAGCACTACTTTACGTCTAGGAAA	660						
QY	661	TTGGTGTCTATAGTCCAGTACATTTGATAAAGCCAGCTTGAATGAATGAATCACTCCAC	720						
DB	661	TTGGTGTCTATAGTCCAGTACATTTGATAAAGCCAGCTTGAATGAATGAATCACTCCAC	720						
QY	721	CAGAAAATATAGAGTCAGTGTCCAAATCAGAACTATGTCTTAAATGGGATTTATACAT	780						
DB	721	CAGAAAATATAGAGTCAGTGTCCAAATCAGAACTATGTCTTAAATGGGATTTATACAT	780						
QY	781	ATGCAAAACATGACTTTTCAAGTTCAAGGTGCGGTCCACGCTTTTAAAGAAAGAACTCTGGAA	840						
DB	781	ATGCAAAACATGACTTTTCAAGTTCAAGGTGCGGTCCACGCTTTTAAAGAAAGAACTCTGGAA	840						
QY	841	ACCATTTGTATAATGGAACAAATACCTGACTGTGAAATGTGAAATGTGAAATGTGAAATGTG	900						
DB	841	ACCATTTGTATAATGGAACAAATACCTGACTGTGAAATGTGAAATGTGAAATGTGAAATGTG	900						

RESULT 2

US-10-824-981-1  
; Sequence 1, Application US/10824981  
; Publication No. US20040191840A1  
; GENERAL INFORMATION:  
; APPLICANT: Benoit, Patrick  
; APPLICANT: Maguire, Deborah  
; APPLICANT: Plavec, Ivan  
; APPLICANT: Tovy, Michael  
; APPLICANT: Meyer, Francois  
; TITLE OF INVENTION: Monoclonal Antibodies Against The Interferon Receptor, With  
; TITLE OF INVENTION: Neutralizing Activity Against Type I Interferon  
; FILE REFERENCE: A-72230-2  
; CURRENT APPLICATION NUMBER: US/10/824,981  
; PRIOR FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US 09/240,675  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: PCT/EP93/00770  
; PRIOR FILING DATE: 1994-12-05  
; PRIOR FILING DATE: 1993-03-30  
; PRIOR APPLICATION NUMBER: EP 92400902.0  
; PRIOR FILING DATE: 1992-03-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1343  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27) .. (1334)  
US-10-824-981-1  
  
Query Match 100.0%; Score 1343; DB 8; Length 1343;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CTGAGGAGATCTGGCGGGCTCCAGATGATGTGCTCTCTCGGGCGGCGACGCCCTAG 60  
|||||

1	CTGCAGGGATCTCGCGCGCTCCAGCATGATGCTGCTCTCTCGGGCGCGACGCCCTAG	60
61	TGCTCTGTCGCGTGGGCCCATGCGTGTGTCGCGAGCCGCGAGTGGAAAAATCTAAAT	120
61	TGCTCTGTCGCGTGGGCCCATGCGTGTGTCGCGAGCCGCGAGTGGAAAAATCTAAAT	120
121	CTCCTCAAAAGTAGAGGTGCGACATCATAGATGACAACCTTTATCTCGAGTGGAAACAGGA	180
121	CTCCTCAAAAGTAGAGGTGCGACATCATAGATGACAACCTTTATCTCGAGTGGAAACAGGA	180
181	CGCATGAGTCTGTCCGGAAATGTCACTTTTCATTTCGATTATCAAAAAATCTGGGATGGATA	240
181	CGCATGAGTCTGTCCGGAAATGTCACTTTTCATTTCGATTATCAAAAAATCTGGGATGGATA	240
241	ATTGGATAAAATGTTCTGGGTGTCAGAAATATTACTATGATACCAAATGCAACTTTCTTCAC	300
241	ATTGGATAAAATGTTCTGGGTGTCAGAAATATTACTATGATACCAAATGCAACTTTCTTCAC	300
301	TCAAGCTGAATGTTTATGAAGAAATTTAAATTTGGGTATTAAGACAGAAAAAGAAAAACATT	360
301	TCAAGCTGAATGTTTATGAAGAAATTTAAATTTGGGTATTAAGACAGAAAAAGAAAAACATT	360
361	CTTCATCGTATGAGTTGATCTATTACACCATTTTCGCAAGCTCAGATTGGTCTCTCCAG	420
361	CTTCATCGTATGAGTTGATCTATTACACCATTTTCGCAAGCTCAGATTGGTCTCTCCAG	420
421	AAGTACATTTAGAACTGGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG	480
421	AAGTACATTTAGAACTGGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG	480
481	ATAGTGTATTGTGGGCTTTGCGATGGTTTAAAGCTTTTACATATAGCTTACTTTCTGGAAAA	540
481	ATAGTGTATTGTGGGCTTTGCGATGGTTTAAAGCTTTTACATATAGCTTACTTTCTGGAAAA	540
541	ACTCTTCAGGTGTAGAAGAAAGGATTCGAAATATTTATTCAGACATATAAATTTATAAAC	600
541	ACTCTTCAGGTGTAGAAGAAAGGATTCGAAATATTTATTCAGACATATAAATTTATAAAC	600
601	TCTCACAGAGACTACTATTGTCTAAAGTTTAAAGCAGCAGCTACTTACGTCTATGGAAAA	660
601	TCTCACAGAGACTACTATTGTCTAAAGTTTAAAGCAGCAGCTACTTACGTCTATGGAAAA	660
661	TTGGTGTCTATAGTCCAGTACATTGTGTATAAGACCAAGTTGAAAAATGAACCTCTCCAC	720
661	TTGGTGTCTATAGTCCAGTACATTGTGTATAAGACCAAGTTGAAAAATGAACCTCTCCAC	720
721	CAGAAATATAGAGTCAAGTGTCCAAATCAGAACCTATGTTCTTAAATGGATTTATACAT	780
721	CAGAAATATAGAGTCAAGTGTCCAAATCAGAACCTATGTTCTTAAATGGATTTATACAT	780
781	ATGCAAAATGACCTTTTCAAGTTCAGTGGCTCCACGCGCTTTTAAAAAGGAATCTCTGGAA	840
781	ATGCAAAATGACCTTTTCAAGTTCAGTGGCTCCACGCGCTTTTAAAAAGGAATCTCTGGAA	840
841	ACCATTTTGTATAATGGAAAAAATACTGTCTGTGAAAAATGTCAAAATCTCCAGTGTG	900
841	ACCATTTTGTATAATGGAAAAAATACTGTCTGTGAAAAATGTCAAAATCTCCAGTGTG	900
901	TCCTTCTCAAAACGTTTTTCAAAAAGGAATTTACCTTCTCCGGTACAGCATCTGATG	960
901	TCCTTCTCAAAACGTTTTTCAAAAAGGAATTTTACCTTCTCCGGTACAGCATCTGATG	960
961	GAAATACACATCTTTTGTGCTCGAAGAGATAAAAGTTTGTATCTGAAATACAAAGCTTTCC	1020
961	GAAATACACATCTTTTGTGCTCGAAGAGATAAAAGTTTGTATCTGAAATACAAAGCTTTCC	1020
1021	TACTTCTCTCCAGTCTTTAAACATTAGATCCCTTCTAGTGAATTCATTCATATCGGTG	1080
1021	TACTTCTCTCCAGTCTTTAAACATTAGATCCCTTCTAGTGAATTCATTCATATCGGTG	1080
1081	CTCCAAAACAGTCTGGAAAAACGCGCTGTGATCCAGGATTTATCCATGATTTATGAATTA	1140
1081	CTCCAAAACAGTCTGGAAAAACGCGCTGTGATCCAGGATTTATCCATGATTTATGAATTA	1140

Qy	1141	TTTTTGGGAAAACACCTTTCAAATGCTCGAGAGAAAAAATTATCGAGAAAAAACTGATGTTA	1201
Db	1141	TTTTTGGGAAAACACCTTTCAAATGCTCGAGAGAAAAAATTATCGAGAAAAAACTGATGTTA	1200
Qy	1201	CAGTTCCTAAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG	1260
Db	1201	CAGTTCCTAAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG	1260
Qy	1261	ATGAAAAGCTGAATPAAAGCAGTGTGTTTTAGTGCACGCTGTATGTGAGAAAACAAAAACAG	1320
Db	1261	ATGAAAAGCTGAATPAAAGCAGTGTGTTTTAGTGCACGCTGTATGTGAGAAAACAAAAACAG	1320
Qy	1321	GAATACCTCTTAATGAGGTACC	1343
Db	1321	GAATACCTCTTAATGAGGTACC	1343
RESULT 3			
US-09-240-675-3			
; Sequence 3, Application US/09240675			
; Patent No. US20020055492A1			
GENERAL INFORMATION:			
; APPLICANT: BENOIT, Patrick			
; APPLICANT: MEYER, Francois			
; APPLICANT: MAGUIRE, Deborah			
; APPLICANT: PLAVEC, Ivan			
; APPLICANT: TOVEY, Michael G.			
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON			
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I			
; NUMBER OF SEQUENCES: 4			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Foley & Lardner			
; STREET: 3000 K Street, N.W., Suite 500			
; CITY: Washington			
; STATE: D.C.			
; ZIP: 20007			
COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)			
CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/240,675			
; FILING DATE:			
PRIOR APPLICATION DATA:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/08/307,588			
; FILING DATE: 05-DEC-1994			
; APPLICATION NUMBER: PCT/EP93/00770			
; FILING DATE: 30-MAR-1993			
PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: EP 92400902.0			
; FILING DATE: 31-MAR-1992			
ATTORNEY/AGENT INFORMATION:			
; NAME: SAXE, Bernhard D.			
; REGISTRATION NUMBER: 28,665			
REFERENCE/DOCKET NUMBER: 17283/117/GUPL			
TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (202)672-5300			
; TELEFAX: (202)672-5399			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1755 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 27..1697			
US-09-240-675-3			

Query Match		99.3%;	Score 1334;	DB 3;	Length 1755;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1334;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CTCGAGGATCTCGGGCGGCTCCAGATGATGGTCGCTCTCTGGGCGGACGACCTAG	60		
DB	1	CTCGAGGATCTCGGGCGGCTCCAGATGATGGTCGCTCTCTGGGCGGACGACCTAG	60		
QY	61	TGCTCGTCGCGCGGCGGCTCCAGATGATGGTCGCTCTCTGGGCGGACGACCTAG	120		
DB	61	TGCTCGTCGCGCGGCGGCTCCAGATGATGGTCGCTCTCTGGGCGGACGACCTAG	120		
QY	121	CTCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA	180		
DB	121	CTCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA	180		
QY	181	GCATGAGTCTGTCGGGAATGTCACCTTTTCATTCGATTCGATTCGATTCGATTCGAT	240		
DB	181	GCATGAGTCTGTCGGGAATGTCACCTTTTCATTCGATTCGATTCGATTCGATTCGAT	240		
QY	241	ATTGGATAAAATGTCGCGGTGTCAGATATTAATAGTACCAATGCAACTTTCTTCAC	300		
DB	241	ATTGGATAAAATGTCGCGGTGTCAGATATTAATAGTACCAATGCAACTTTCTTCAC	300		
QY	301	TCAAGCTGAATGTTATGAAGAAATTAATTTGCGTATAGAGCAGAGAAAGAAACACTT	360		
DB	301	TCAAGCTGAATGTTATGAAGAAATTAATTTGCGTATAGAGCAGAGAAAGAAACACTT	360		
QY	361	CTTCATGATGAGTGTGCTCACTTTACACCATTTCCGAAAGCTCAGATTTGCTCCAG	420		
DB	361	CTTCATGATGAGTGTGCTCACTTTACACCATTTCCGAAAGCTCAGATTTGCTCCAG	420		
QY	421	AAGTACATTTAGAGCTGAAGATAAGCAATAGTGATACACATCTCTCTGGGAAACAAAG	480		
DB	421	AAGTACATTTAGAGCTGAAGATAAGCAATAGTGATACACATCTCTCTGGGAAACAAAG	480		
QY	481	ATAGTGTATGTCGGCTTTGAGTGTGTTAAGCTTTACATATAGCTTACTTTATCTGAAA	540		
DB	481	ATAGTGTATGTCGGCTTTGAGTGTGTTAAGCTTTACATATAGCTTACTTTATCTGAAA	540		
QY	541	ACTCTTCAGTGTAGAGAAAGATTCGAAATATTTATTCAGACATATAATTTATAAC	600		
DB	541	ACTCTTCAGTGTAGAGAAAGATTCGAAATATTTATTCAGACATATAATTTATAAC	600		
QY	601	TCTCACCAGAGACTACTTTATGCTAAAGCTTAAAGCAGCACTACTTTACGTCATGAAA	660		
DB	601	TCTCACCAGAGACTACTTTATGCTAAAGCTTAAAGCAGCACTACTTTACGTCATGAAA	660		
QY	661	TTGGTGTCTATAGTCCAGTACATTTGTATAAAGACCACAGTTGAAATGAACTACCTCCAC	720		
DB	661	TTGGTGTCTATAGTCCAGTACATTTGTATAAAGACCACAGTTGAAATGAACTACCTCCAC	720		
QY	721	CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTTACAT	780		
DB	721	CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTTACAT	780		
QY	781	ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAGAAAGAAATCTGGAA	840		
DB	781	ATGCAAAACATGACCTTTCAAGTTCAGTGGCTCCAGCGCTTTTAAAGAAAGAAATCTGGAA	840		
QY	841	ACCATTTGTATAATGAAAACAAATACCTGACTGTGAAAATGTCAAAACCTACCCAGTGTG	900		
DB	841	ACCATTTGTATAATGAAAACAAATACCTGACTGTGAAAATGTCAAAACCTACCCAGTGTG	900		
QY	901	TCCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGCGTACAGCATCTGATG	960		
DB	901	TCCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGCGTACAGCATCTGATG	960		
QY	961	GAAATAACACATCTTTTGTGCTGAAGAGATAAAGTTTGATGCTGAAAATAAGAGCTTTCC	1020		
DB	961	GAAATAACACATCTTTTGTGCTGAAGAGATAAAGTTTGATGCTGAAAATAAGAGCTTTCC	1020		
QY	1021	TACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCATTCATATCTATATCGGTG	1080		

DB	1021	TACTTCTCCAGTCTTTAAACATTTAGATCCCTTAGTGATTCATTCATATCTATATCGGTG	1080		
QY	1081	CTCCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTACCTGATTTATGAATTA	1140		
DB	1081	CTCCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTACCTGATTTATGAATTA	1140		
QY	1141	TTTTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTTATCGAGAAAACCTGATGTTA	1200		
DB	1141	TTTTTTGGGAAAACACTTCAAAATGCTGAGAGAAAATTTATCGAGAAAACCTGATGTTA	1200		
QY	1201	CAGTTCCTAATTTGAAAACCACTGACTGTATATTTGTGTGAAAGCCAGACACACCATGG	1260		
DB	1201	CAGTTCCTAATTTGAAAACCACTGACTGTATATTTGTGTGAAAGCCAGACACACCATGG	1260		
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QY	1321	GAAATACCTCTAAA 1334			
DB	1321	GAAATACCTCTAAA 1334			
RESULT 4					
US-10-824-981-3					
; Sequence 3, Application US/10824981					
; Publication No. US20040191840A1					
; GENERAL INFORMATION:					
; APPLICANT: Benoit, Patrick					
; APPLICANT: Maguire, Deborah					
; APPLICANT: Plavec, Ivan					
; APPLICANT: Tovy, Michael					
; APPLICANT: Meyer, Francois					
; TITLE OF INVENTION: Monoclonal Antibodies Against The Interferon Receptor, With					
; FILE OF INVENTION: Neutralizing Activity Against Type I Interferon					
; FILE REFERENCE: A-72230-2					
; CURRENT FILING DATE: 2004-04-14					
; PRIOR APPLICATION NUMBER: US/10/824,981					
; PRIOR FILING DATE: 1999-02-02					
; PRIOR APPLICATION NUMBER: US 08/307,588					
; PRIOR FILING DATE: 1994-12-05					
; PRIOR APPLICATION NUMBER: PCT/EP93/00770					
; PRIOR FILING DATE: 1993-03-30					
; PRIOR APPLICATION NUMBER: EP 92400902.0					
; PRIOR FILING DATE: 1992-03-31					
; NUMBER OF SEQ ID NOS: 4					
; SOFTWARE: PatentIn version 3.2					
; SEQ ID NO 3					
; LENGTH: 1755					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
; FEATURE:					
; NAME/KEY: CDS					
; LOCATION: (27)..(1697)					
US-10-824-981-3					
Query Match					
Best Local Similarity 99.2%; Score 1332.4; DB 8; Length 1755;					
Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	1	CTGCGAGGATCTCGCGCGGCTCCAGATGATGGTCGCTCTCTGGGCGGACGACCTAG	60		
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QY	61	TGCTCGTCGCGCGGCGGCTCCAGATGATGGTCGCTCTCTGGGCGGACGACCTAG	120		
DB	61	TGCTCGTCGCGCGGCGGCTCCAGATGATGGTCGCTCTCTGGGCGGACGACCTAG	120		
QY	121	CTCCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA	180		
DB	121	CTCCTCAAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA	180		



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Qy 181 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240
Db 181 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240
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Db 241 ATTGGATAAATCTCTGGGTGTCAGATATATCTAGTACCAATGCAATCTTCTTCAC 300
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGAGCAGAAAAAGAAACACTT 360
Db 301 TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGAGCAGAAAAAGAAACACTT 360
Qy 361 CTTCAATGATGAGGTGACTCATTTACACCAATTCGCAAAAGCTCAGATTGGTCTCCAG 420
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Qy 541 ACTCTTCAGGTGTAGAAGAAAGGATTGAAAAATATTTATTCAGACATAAAAAATTTATAAC 600
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Qy 601 TCTCACCAGAGACTACTTATTTGTCTAAAGTTAAAGCAGACACTACTTACGTCTATGGAATA 660
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Db 661 TTGTTGCTATAGTCCAGTACATTTGTATAAGACACAGATTGAAATGAACTACTCTCCAC 720
Qy 721 CAGAAAAATATAGAGTCAAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATATATCAT 780
Db 721 CAGAAAAATATAGAGTCAAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATATATCAT 780
Qy 781 ATGCAAAACATGACCTTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAAAGGAATCTCGAA 840
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Qy 841 ACCATTTGTAATAATGGAAAAAATACTGACTGTGAAAAATGTCAAAACTACCCAGTGTG 900
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Qy 901 TCTTTCTCAAAACGTTTTCCAAAAGGAATTTACCTTCTCGCGGTACAAGCATCTGATG 960
Db 901 TCTTTCTCAAAACGTTTTCCAAAAGGAATTTACCTTCTCGCGGTACAAGCATCTGATG 960
Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATAACAAGCTTTCC 1020
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Qy 1021 TACTTCTCTCCAGTCTTTAAACATTAGATCCCTTAGTGTATTCATTCATATCTATATCGGTG 1080
Db 1021 TACTTCTCTCCAGTCTTTAAACATTAGATCCCTTAGTGTATTCATTCATATCTATATCGGTG 1080
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Db 1081 CTCCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA 1140
Qy 1141 TTTTGGGAAAAACACTTCAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200
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Qy 1261 ATGAAAAGCTGAATAAAGCAGTGTTTTATGTCGCTGTATGTGAGAAAAACAAACCCAG 1320
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Qy 1321 GAAATACCTCTAAA 1334
Db 1321 GAAATACCTCTAAA 1334

RESULT 5
US-10-641-643-1118
; Sequence 1118, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2755 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g184645
; SEQUENCE DESCRIPTION: SEQ ID NO: 1118 :
US-10-641-643-1118

Query Match 99.1%; Score 1330.8; DB 7; Length 2755;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCGAGGATCTGCGGGGCTCCAGATGATGGTCTCTCTGCGCGCGAGCCCTAG 60
Db 53 CTGCTGGGATCTGCGGGGCTCCAGATGATGGTCTCTCTGCGCGCGAGCCCTAG 112
Qy 61 TGCTCGTCCGCTGGGCCCATGGGTGTTGTCGCGAGCCGAGGTGGAATAATCTAAAT 120
Db 113 TGCTCGTCCGCTGGGCCCATGGGTGTTGTCGCGAGCCGAGGTGGAATAATCTAAAT 172
Qy 121 CTCCTCAAAAAGTAGAGTTCGACATCATAGATGACAACTTTTATCTGAGGTGGAAACAGGA 180
Db 173 CTCCTCAAAAAGTAGAGTTCGACATCATAGATGACAACTTTTATCTGAGGTGGAAACAGGA 232
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181 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTCGATTATCAAAAAAAGTGGATGGATA 240  
Db GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTCGATTATCAAAAAAAGTGGATGGATA 292  
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QY 301 TCAAGCTGAATGTTTATGAGAAATTAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 360  
Db 353 TCAAGCTGAATGTTTATGAGAAATTAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 412  
QY 361 CTTCAATGGTATGAGTTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
Db 413 CTTCAATGGTATGAGTTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 472  
QY 421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTGGAAACAAAAG 480  
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QY 481 ATAGTGTATGTGGCTTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 540  
Db 533 ATAGTGTATGTGGCTTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 592  
QY 541 ACTCTTCAGGTGTAGAGAAAGGATTGAAATATTTATTCAGACATATAAAATTTATAAAC 600  
Db 593 ACTCTTCAGGTGTAGAGAAAGGATTGAAATATTTATTCAGACATATAAAATTTATAAAC 652  
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QY 661 TTGTGTCTATAGTCCAGTACATTGTATAAGACACAGTTGAAATGAAATGAACTACCTCCAC 720  
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QY 721 CAGAAAAATATAGAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780  
Db 773 CAGAAAAATATAGAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTATACAT 832  
QY 781 ATGCAACATGACCTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGGAATCTCGGAA 840  
Db 833 ATGCAACATGACCTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGGAATCTCGGAA 892  
QY 841 ACCAATTGTATAAATGAAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900  
Db 893 ACCAATTGTATAAATGAAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 952  
QY 901 TCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTTCTCCGCTACAGCATCTGATG 960  
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QY 961 GAAATAACACATCTTTTGTCTGAGAGATAAAGTTTGTACTGAAATACAGACTTTTC 1020  
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Db 1073 TACTTCTCCAGTCTTAAACATTTAGATCCCTTGTAGTATTCATTCATATCTATCGGTG 1132  
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Db 1133 CTCAAAAACAGTCTGAAAAACAGCCTGTGTATCCAGGATTTATCCATGATTTATGAAATTA 1192  
QY 1141 TTTTGTGGGAAAAACATTTCAATTCGTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
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QY 1201 CAGTCTCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGACACACCATGG 1260  
Db 1253 CAGTCTCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGACACACCATGG 1312

QY 1261 ATGAAAGCTGAATAAAAGCAGTGTGTTTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
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QY 1321 GAAATACCTCTAAA 1334  
Db 1373 GAAATACCTCTAAA 1386  
RESULT 6  
US-10-888-313A-81  
; Sequence 81, Application US/10888313A  
; Publication No. US20050100934A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, Kevin  
; APPLICANT: AXEL, Richard  
; APPLICANT: STRAPPS, Walter  
; APPLICANT: BARNEA, Gilad  
; TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction  
; FILE REFERENCE: SENTI 203.2  
; CURRENT APPLICATION NUMBER: US/10/888,313A  
; PRIOR FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: 60/566,113  
; PRIOR FILING DATE: 2004-04-27  
; PRIOR APPLICATION NUMBER: 60/511,918  
; PRIOR FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/485,968  
; PRIOR FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 101  
; SEQ ID NO 81  
; LENGTH: 2755  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-888-313A-81  
Query Match 99.1%; Score 1330.8; DB 9; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CTGACGGATCTCGCGGGCTCCAGATGATGGTCTCTCTGGGGCGGACACCCCTAG 60  
Db 53 CTGCTGGGATCTCGCGGGCTCCAGATGATGGTCTCTCTGGGGCGGACACCCCTAG 112  
QY 61 TGCTCTCCCGCTGGGCCCATGGTCTGTCGCGAGCCGAGGTGAAATAATCTAAAT 120  
Db 113 TGCTCTCCCGCTGGGCCCATGGTCTGTCGCGAGCCGAGGTGAAATAATCTAAAT 172  
QY 121 CTCCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTGAGTGGAACAGGA 180  
Db 173 CTCCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTCTGAGTGGAACAGGA 232  
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Db 233 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTCGATTATCAAAAAAAGTGGATGGATA 292  
QY 241 ATTGGATAAAATTCGTGCGGTGTGAGATATTACTAGTACCAATGCAACTTTTCTTCAC 300  
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QY 361 CTTCAATGGTATGAGTTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
Db 413 CTTCAATGGTATGAGTTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 472  
QY 421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTGGAAACAAAAG 480  
Db 473 AAGTACATTTAGAGCTGAAGATAGGCAATAGTGATACACATCTCTCTGGAAACAAAAG 532  
QY 481 ATAGTGTATGTGGCTTTTGGATGGTTTAAAGCTTTACATATAGCTTACTTATCTGAAAA 540

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601	TCTCACAGAGACTACTATTATTTGCTCTAAAGTTAAAGCAGCAGCTACTTTACGTCTATGGAAAA	660
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661	TTGGTGTCTATAGTCCAGTACATTTGTATATAAGACCACAGTGTGAAAAATGAATACCTCCAC	720
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833	ATGCAAACTAGCACTTTTCAAGTTCAGTGGCTCCACGCTTTTAAAAAGGAATCCTCGAA	892
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893	ACCATTGTTATAATGGAAAACAAATACCTGACTGTGAAAAATGTCAAACACTACCCAGTGTG	952
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1133	CTCCAAAAACAGTCTGGAAAAACAGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA	1192
1141	TTTTTTTGGAAAAACACTTCAAATGCTGAGAGAAAAATATTCGAGAAAAAAACTGATGTTA	1200
1193	TTTTTTTGGAAAAACACTTCAAATGCTGAGAGAAAAATATTCGAGAAAAAAACTGATGTTA	1252
1201	CAGTTCCTTAATTTCAAAACCACTGATATATCTGTGTAAGCCAGAGCCACACCACTGG	1260
1253	CAGTTCCTTAATTTCAAAACCACTGATATATCTGTGTAAGCCAGAGCCACACCACTGG	1312
1261	ATGAAAAAGCTGAATATAAAGCAGTGTTTTTTAGTGACGCTGTATGTGAGAAAAACAAACCG	1320
1313	ATGAAAAAGCTGAATATAAAGCAGTGTTTTTTAGTGACGCTGTATGTGAGAAAAACAAACCG	1372
1321	GAATATACCTCTTAAA	1334
1373	GAATATACCTCTTAAA	1386

## RESULT 7

US-09-925-300-732	
Sequence 732, Application US/09925300	
Patent No. US20020151681A1	
GENERAL INFORMATION:	
APPLICANT: Craig Rosen,	
APPLICANT: Steve Ruben	
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies	
FILE REFERENCE: PA101	
CURRENT APPLICATION NUMBER: US/09/925,300	
CURRENT FILING DATE: 2001-08-10	
PRIOR APPLICATION NUMBER: PCT/US00/05988	
PRIOR FILING DATE: 2000-03-08	
PRIOR APPLICATION NUMBER: 60/124,270	

Qy 901 TCTTCTCAAAACGTTTTCCAAAAGGAAATTTACCTTCTCCGGTACAAGCATCTGATG 960  
Db 959 TCTTCTCAAAACGTTTTCCAAAAGGAAATTTACCTTCTCCGGTACAAGCATCTGATG 1018  
Qy 961 GAAATACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTAGTAAATCAAGCTTTCC 1020  
Db 1019 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTAGTAAATCAAGCTTTCC 1078  
Qy 1021 TACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGTGATTCATTCCATATCTATATCGGTG 1080  
Db 1079 TACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGTGATTCATTCCATATCTATATCGGTG 1138  
Qy 1081 CTCAAAACAGTCTGGAACAACGCTCTGTATCCAGGATTTCCACTGATTTATGAATTA 1140  
Db 1139 CTCAAAACAGTCTGGAACAACGCTCTGTATCCAGGATTTCCACTGATTTATGAATTA 1198  
Qy 1141 TTTTGGGAAACACATTTCAAATGCTGAGAGAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Db 1199 TTTTGGGAAACACATTTCAAATGCTGAGAGAAAATTTATCGAGAAAAAACTGATGTTA 1258  
Qy 1201 CAGTTCCTAAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1260  
Db 1259 CAGTTCCTAAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1318  
Qy 1261 ATGAAAAGCTGAATAAAGCAGTGTGTTTATGTCAGCGCTGTATGTGAGAAAAACAAACAG 1320  
Db 1319 ATGAAAAGCTGAATAAAGCAGTGTGTTTATGTCAGCGCTGTATGTGAGAAAAACAAACAG 1378  
Qy 1321 GAAATACCTTAA 1334  
Db 1379 GAAATACCTTAA 1392

RESULT 8

US-09-822-830A-38/c  
; Sequence 38, Application US/09822830A  
; Patent No. US20020142952A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics Institute, Inc.  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.  
; APPLICANT: Gulukota, Kamalakar  
; APPLICANT: Graham, James R.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
; FILE REFERENCE: GIN 6402  
; CURRENT APPLICATION NUMBER: US/09/822,830A  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/195,604  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 631  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 2278  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-822-830A-38

Query Match 98.7%; Score 1326; DB 3; Length 2278;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1329; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CTGAGGATCTCGCGCGTCCAGATGATGTCGTCCTCGGGCGGACGACCCCTAG 60  
Db 2213 CTGAGGATCTCGCGCGTCCAGATGATGTCGTCCTCGGGCGGACGACCCCTAG 2154  
Qy 61 TGCTCGTCGCGTGGGCCCATGGTGTGTCGCGAGCCGAGGTGGAAAAAATCTAAAT 120  
Db 2153 TGCTCGTCGCGTGGGCCCATGGTGTGTCGCGAGCCGAGGTGGAAAAAATCTAAAT 2094

Qy 121 CTCCTCAAAAAGTAGAGTCCGATCATAGATGACAACTTTATCTCTGAGTGGAAACAGGA 180  
Db 2093 CTCCTCAAAAAGTAGAGTCCGATCATAGATGACAACTTTATCTCTGAGTGGAAACAGGA 2034  
Qy 181 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTTCGATTATCAAAAAAACTGGGATGATA 240  
Db 2033 GCGATGAGTCTGTGCGGAATGTGACTTTTTCATTTCGATTATCAAAAAAACTGGGATGATA 1974  
Qy 241 ATTGGATAAAATTTGCTCGGTGTGAGATATTTACATAGTACCAATGCAATCTTTCTTCAC 300  
Db 1973 ATTGGATAAAATTTGCTCGGTGTGAGATATTTACATAGTACCAATGCAATCTTTCTTCAC 1914  
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTTAAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 360  
Db 1913 TCAAGCTGAATGTTTATGAAGAAATTTAAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 1854  
Qy 361 CTTTCATGATGAGGTTGACTCATTTTACACCAATTTCCGAAAGCTCAGATTGGTCTCCAG 420  
Db 1853 CTTTCATGATGAGGTTGACTCATTTTACACCAATTTCCGAAAGCTCAGATTGGTCTCCAG 1794  
Qy 421 AAGTACATTTAGAGCTGGAAGTAAAGCAATAGTGATACACATCTCTCTCGGACCAAAAG 480  
Db 1793 AAGTACATTTAGAGCTGGAAGTAAAGCAATAGTGATACACATCTCTCTCGGACCAAAAG 1734  
Qy 481 ATAGTGTATGTGGGCTTTGGATGTTTAAAGCTTTACATATAGCTTTACTTTATCTGAAAA 540  
Db 1733 ATAGTGTATGTGGGCTTTGGATGTTTAAAGCTTTACATATAGCTTTACTTTATCTGAAAA 1674  
Qy 541 ACTTTTCAGGTGTAAGAAAGATTGAAAAATATTTTATTCAGACATAAAATTTATAAAC 600  
Db 1673 ACTTTTCAGGTGTAAGAAAGATTGAAAAATATTTTATTCAGACATAAAATTTATAAAC 1614  
Qy 601 TCTCACGAGACTACTTATTTCTTAAAGTTTAAAGCAGCAGCTACTTACGTGATGAAAA 660  
Db 1613 TCTCACGAGACTACTTATTTCTTAAAGTTTAAAGCAGCAGCTACTTACGTGATGAAAA 1554  
Qy 661 TTGGTGTCTATAGTCCAGTACATTTGTATAAAGACACACAGTTGAAAAATGAATACCTCCAC 720  
Db 1553 TTGGTGTCTATAGTCCAGTACATTTGTATAAAGACACAGTTGAAAAATGAATACCTCCAC 1494  
Qy 721 CAGAAAAATAGAAGTCAAGTCCAAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
Db 1493 CAGAAAAATAGAAGTCAAGTCCAAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 1434  
Qy 781 ATGCAAAACATGACCTTTCAAGTTCAGTGCGTCCAGCCCTTTTAAAAAGGAATCTCGGA 840  
Db 1433 ATGCAAAACATGACCTTTCAAGTTCAGTGCGTCCAGCCCTTTTAAAAAGGAATCTCGGA 1374  
Qy 841 ACCATTTGTATAAATGGAACAAATACCTGACTGTGAAAAATGTCAAAACTTACCAGTGTG 900  
Db 1373 ACCATTTGTATAAATGGAACAAATACCTGACTGTGAAAAATGTCAAAACTTACCAGTGTG 1314  
Qy 901 TCTTCTCAAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCGCGGTACAGCATCTGATG 960  
Db 1313 TCTTCTCAAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCGCGGTACAGCATCTGATG 1254  
Qy 961 GAAATAACACATCTTTTTCGCTGGAAGAGATAAAGTTTGCATCTGAAAAATACAGCTTTCC 1020  
Db 1253 GAAATAACACATCTTTTTCGCTGGAAGAGATAAAGTTTGCATCTGAAAAATACAGCTTTCC 1194  
Qy 1021 TACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGTGATTCATTTCATATCTATATCGGTG 1080  
Db 1193 TACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGTGATTCATTTCATATCTATATCGGTG 1134  
Qy 1081 CTCAAAAACAGTCTGAAAAACGCGCTGTATCCAGGATTTACCATGATTTATGAATTA 1140  
Db 1133 CTCAAAAACAGTCTGAAAAACGCGCTGTATCCAGGATTTATCCCATGATTTATGAATTA 1074  
Qy 1141 TTTTGGGAAACACCTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Db 1073 TTTTGGGAAACACCTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1014  
Qy 1201 CAGTTCCTAAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1260

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Db 1013 CAGTTCCTAAATTTGAAACCACTGACTGCTATATTTGTGTGAAGCCAGAGCACAACCATGG 954
Qy 1261 ATGAAAAGCTGAATATAAAGCAGTGTGTTTTAGTGCAGCTGTATGTGAGAAAAACAAAACAG 1320
Db 953 ATGAAAAGCTGAATATAAAGCAGTGTGTTTTAGTGCAGCTGTATGTGAGAAAACAAAACAG 894
Qy 1321 GAAATACCTCTAAA 1334
Db 893 GAAATACCTCTAAA 880

RESULT 9
US-10-764-833-43
; Sequence 43, Application US/10764833
; Publication No. US20040248157A1
; GENERAL INFORMATION:
; APPLICANT: Ayalon, Michal
; APPLICANT: Pollock, Sarah
; APPLICANT: Diber, Alex
; APPLICANT: Levine, Zurit
; APPLICANT: Nemzer, Sergey
; APPLICANT: Dahary, Dvir
; APPLICANT: Sorek, Rotem
; APPLICANT: Levanon, Erez
; APPLICANT: Rotman, Galit
; APPLICANT: Savitsky, Kineret
; APPLICANT: Chermesh, Chen
; APPLICANT: Mintz, Liat
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING SOLUBLE POLYPEPTIDES AND METHODS
; FILE OF INVENTION: SAME
; FILE REFERENCE: 27256
; CURRENT APPLICATION NUMBER: US/10/764,833
; CURRENT FILING DATE: 2004-01-27
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-764-833-43

Query Match 97.8%; Score 1313.2; DB 8; Length 1512;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1318; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CTGAGGGATCTGGGGCGCTCCAGATGATGGTCTCTCTGGCGGCGAGCCCTAG 60
Db 127 CTGTGGGATCTGGCGGGCTCCAGATGATGGTCTCTCTGGCGGCGAGCCCTAG 186
Qy 61 TGCTCGTCGCGTGGGCGCATGGGTGTTGTCGAGCGCGCAGGTGGAATAATCTAAAAT 120
Db 187 TGCTCGTCGCGTGGGCGCATGGGTGTTGTCGAGCGCGCAGGTGGAATAATCTAAAAT 246
Qy 121 CTCTCAAAAAGTAGAGGTGCAATCATAGATGACAACCTTTATCTGAGGTGGAAACAGGA 180
Db 247 CTCCTCAAAAAGTAGAGGTGCAATCATAGATGACAACCTTTATCTGAGGTGGAAACAGGA 306
Qy 181 GCGATGAGTCTGCGGGAATGATGATTTTTCATTCGATTATCAAAAACCTGGGATGGATA 240
Db 307 GCGATGAGTCTGCGGGAATGATGATTTTTCATTCGATTATCAAAAACCTGGGATGGATA 366
Qy 241 ATTGATATAAATGCTCGGGTGTGAGATATTTACTAGTACCAATGCAACTTTCTCTCAC 300
Db 367 ATTGATATAAATGCTCGGGTGTGAGATATTTACTAGTACCAATGCAACTTTCTCTCAC 426
Qy 301 TCAAGCTGAAATGTTTATGAAGAAATTTAAATTCGGTATTAAGACGAGAAAAAACAACATT 360
```

RESULT 10

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Db 427 TCAAGCTGAAATGTTTATGAAGAAATTTAAATTCGGTATTAAGACGAGAAAAACAACATT 486
Qy 361 CTTTCATGTTATGAGGTGACTCAATTTTACACCAATTTGCAAAAGCTCAGATTTGGTCTCCAG 420
Db 487 CTTTCATGTTATGAGGTGACTCAATTTTACACCAATTTGCAAAAGCTCAGATTTGGTCTCCAG 546
Qy 421 AAGTACATTTTGAAGCTGAAGATAAGGCATAGGTATACACATCTCTCTCGGAACAAAAG 480
Db 547 AAGTACATTTTGAAGCTGAAGATAAGGCATAGGTATACACATCTCTCTCGGAACAAAAG 606
Qy 481 ATAGTGTATGTCGGGCTTTTGGATGGTTTAAAGCTTTTACATATAGCTTACTTTATCTGAAAA 540
Db 607 ATAGTGTATGTCGGGCTTTTGGATGGTTTAAAGCTTTTACATATAGCTTACTTTATCTGAAAA 666
Qy 541 ACTCTTCAGGTGTAGAAGAAAGGATTTGAAAATATTTTATTCAGACATATAAATTTTATAAAC 600
Db 667 ACTCTTCAGGTGTAGAAGAAAGGATTTGAAAATATTTTATTCAGACATATAAATTTTATAAAC 726
Qy 601 TCTCACCAGAGACTACTTATTGTTCTAAAAGCTTAAAGCAGCAGCTACTTACGTTCATGGAAAA 660
Db 727 TCTCACCAGAGACTACTTATTGTTCTAAAAGCTTAAAGCAGCAGCTACTTACGTTCATGGAAAA 786
Qy 661 TTGGTGTCTATAGTCCAGTACATTTGTATAAAGACACAGATTGAAAAATGAACACTACTCCAC 720
Db 787 TTGGTGTCTATAGTCCAGTACATTTGTATAAAGACACAGATTGAAAAATGAACACTACTCCAC 846
Qy 721 CAGAAAAATATAGAAGTCAGTGTCCAAAATCAGAACTAATGTTCTTTAAATGGGATTTATCAT 780
Db 847 CAGAAAAATATAGAAGTCAGTGTCCAAAATCAGAACTAATGTTCTTTAAATGGGATTTATCAT 906
Qy 781 ATGCAAAACATGACCTTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGAGGAAATCCTGGAA 840
Db 907 ATGCAAAACATGACCTTTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAGAGGAAATCCTGGAA 966
Qy 841 ACCATTTGTATAAATGAAGCAAAATACCTGACTGTGAAAAATGTCAAAATACCAAGCTGTG 900
Db 967 ACCATTTGTATAAATGAAGCAAAATACCTGACTGTGAAAAATGTCAAAATACCAAGCTGTG 1026
Qy 901 TCTTTCTCTCAAAACGTTTTTCCAAAAGGAAATTTACCTTCTCCGCGTCAAGCATCTGATG 960
Db 1027 TCTTTCTCTCAAAACGTTTTTCCAAAAGGAAATTTACCTTCTCCGCGTCAAGCATCTGATG 1086
Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAAAGCTTTCC 1020
Db 1087 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAAAGCTTTCC 1146
Qy 1021 TACTTCTCTCAGTCTTTAAACATTAAGATCCCTTAGTGATTCAATCCATATCTATATCGGTG 1080
Db 1147 TACTTCTCTCAGTCTTTAAACATTAAGATCCCTTAGTGATTCAATCCATATCTATATCGGTG 1206
Qy 1081 CTCCAAAACAGTCTGGAAAAACACGCTGTGTATCCAGGATTTATCCATGTTTATGAAATTA 1140
Db 1207 CTCCAAAACAGTCTGGAAAAACACGCTGTGTATCCAGGATTTATCCATGTTTATGAAATTA 1266
Qy 1141 TTTTGTGGAAAAACATTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAAACTGATGTTA 1200
Db 1267 TTTTGTGGAAAAACATTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAAACTGATGTTA 1326
Qy 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACATGG 1260
Db 1327 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACATGG 1386
Qy 1261 ATGAAAAGCTGAATATAAAGCAGTGTGTTTTTAGTGCAGCTGTATGTGAGAAAAACAAAACAG 1320
Db 1387 ATGAAAAGCTGAATATAAAGCAGTGTGTTTTTAGTGCAGCTGTATGTGAGAAAAACAAAACAG 1446
Qy 1321 GAAATA 1326
Db 1447 GTCAGA 1452
```

Db	740	CTCTCACGAGACTACTTATTGCTCTAAAAAGTTAAAGCAGCACTACTTACGTCTATGGAAA	799
Qy	660	ATTGGTGTCTATAGTCCAGTACACATCTGTATAAGACGACACAGTTCGAAATGAACCTACCTCCA	719
Db	800	ATTGGTGTCTATAGTCCAGTACACATCTGTATAAGACGACACAGTTCGAAATGAACCTACCTCCA	859
Qy	720	CCAGAAATATAGAAGTCAGTGTCCAAATATCAGAACTATGTTCTTAAATGGGAATATATACA	779
Db	860	CCAGAAATATAGAAGTCAGTGTCCAAATATCAGAACTATGTTCTTAAATGGGAATATATACA	919
Qy	780	TATGCAAAATGACCTTTTCAAGTTCAGTGGCTCCACGCCCTTTTAAAGGAATCTCTGGA	839
Db	920	TATGCAAAATGACCTTTTCAAGTTCAGTGGCTCCACGCCCTTTTAAAGGAATCTCTGGA	979
Qy	840	AACCATTTGTATAAATGGAACCAAAATACCTGACGTGTGAATATGTCAAACTACCCAGTGT	899
Db	980	AACCATTTGTATAAATGGAACCAAAATACCTGACGTGTGAATATGTCAAACTACCCAGTGT	1039
Qy	900	GTCTTTCTCTCAAAACGTTTTTCCAAAAGGAATTTTACCTTCTCCGCGCTACAAAGCATCTGAT	959
Db	1040	GTCTTTCTCTCAAAACGTTTTTCCAAAAGGAATTTTACCTTCTCCGCGCTACAAAGCATCTGAT	1099
Qy	960	GGAAATAACACATCTTTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATPACAAGCTTTC	1019
Db	1100	GGAAATAACACATCTTTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATPACAAGCTTTC	1159
Qy	1020	CTACTTCTCTCCAGTCTTTAAATAGATCCCTTAGTGAATTCATTCATATCTATATCGGT	1079
Db	1160	CTACTTCTCTCCAGTCTTTAAATAGATCCCTTAGTGAATTCATTCATATCTATATCGGT	1219
Qy	1080	GCTCCAAAACAGTCTGGAAACAGCCTGTGTATCCAGGATTTATCCACTGATTTTATGAAATT	1139
Db	1220	GCTCCAAAACAGTCTGGAAACAGCCTGTGTATCCAGGATTTATCCACTGATTTTATGAAATT	1279
Qy	1140	ATTTTTTGGAAAACACTTCCAAATGCTGAGAGAAAAAATTTATCGAGAAAAAACTGATGTT	1199
Db	1280	ATTTTTTGGAAAACACTTCCAAATGCTGAGAGAAAAAATTTATCGAGAAAAAACTGATGTT	1339
Qy	1200	ACAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGTAAGCCAGACACACACCATG	1259
Db	1340	ACAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGTAAGCCAGACACACACCATG	1399
Qy	1260	GATGAAAAGCTGAATATAAGACAGTGTTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCA	1319
Db	1400	GATGAAAAGCTGAATATAAGACAGTGTTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCA	1459
Qy	1320	GGAAATACCTCTTAAA	1334
Db	1460	GGAAATACCTCTTAAA	1474

RESULT 11

US-10-027-632-118153

; Sequence 118153, Application US/10027632

; Publication No. US20020198371A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 118153  
;; LENGTH: 1035  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-118153

Query Match 13.6%; Score 182.2; DB 5; Length 1035;  
Best Local Similarity 93.6%; Pred. No. 1.8e-36;  
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 265  
Db TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 246  
Qy 266 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325  
Db GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306  
Qy 326 TAAATTGCGTATAGACGAGCAAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 385  
Db TAAATTGCGTATAGACGAGCAAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 366  
Qy 386 TACACCATTTTCGCAAAAGCTCAGA 408  
Db TACACCATTTTCGCAAAAGGTAAGA 389

RESULT 12  
US-10-027-632-118154  
; Sequence 118154, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 118154  
; LENGTH: 1035  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-118154

Query Match 13.6%; Score 182.2; DB 5; Length 1035;  
Best Local Similarity 93.6%; Pred. No. 1.8e-36;  
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 265  
Db TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 246

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 265  
Db TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 246

Qy 266 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325  
Db GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306  
Qy 326 TAAATTGCGTATAGACGAGCAAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 385  
Db TAAATTGCGTATAGACGAGCAAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 366  
Qy 386 TACACCATTTTCGCAAAAGCTCAGA 408  
Db TACACCATTTTCGCAAAAGGTAAGA 389

RESULT 13  
US-10-027-632-118153  
; Sequence 118153, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 118153  
; LENGTH: 1035  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-118153

Query Match 13.6%; Score 182.2; DB 6; Length 1035;  
Best Local Similarity 93.6%; Pred. No. 1.8e-36;  
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 206 TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 265  
Db TTTTTCATTGATTAACAAAACCTGGGATGATAAATGGATAAAATGTCGGGTGTCA 246  
Qy 266 GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325  
Db GAATATTACTAGTACCAAAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306  
Qy 326 TAAATTGCGTATAGACGAGCAAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 385  
Db TAAATTGCGTATAGACGAGCAAAAAGAAAACACTTCTTCATGTTGATGAGGTTGACTCATT 366  
Qy 386 TACACCATTTTCGCAAAAGCTCAGA 408  
Db TACACCATTTTCGCAAAAGGTAAGA 389

RESULT 14  
US-10-027-632-118154  
; Sequence 118154, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
POLYMORPHISMS IN THE HUMAN GENOME  
FILE REFERENCE: 108827-129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 118154  
LENGTH: 1035  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-118154

Query Match 13.6%; Score 182.2; DB 6; Length 1035;  
Best Local Similarity 93.6%; Pred. No. 1.8e-36;  
Matches 190; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 206 TTTTTCATTCGATTATCAAAATACTGGGATGGATAATTGGATAAAATTTGTCGGGTGCA 265  
DB 187 TTTGTTTTTTTACTTTAAAGAACTGGGATGGATAATTGGATAAAATTTGTCGGGTGCA 246  
QY 266 GAATATTACTAGTACCAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 325  
DB 247 GAATATTACTAGTACCAATGCAACTTTTCTCACTCAAGCTGAATGTTTATGAAGAAAT 306  
QY 326 TAAATTGCGTATAGAGCAGAAAAGAAACACTTCTTCATGTTATGAGTTGACTCATT 385  
DB 307 TAAATTGCGTATAGAGCAGAAAAGAAACACTTCTTCATGTTATGAGTTGACTCATT 366  
QY 386 TACACCATTTGCAAAAGCTCAGA 408  
DB 367 TACACCATTTGCAAAAGCTAAGA 389

RESULT 15  
US-10-450-763-17284  
Sequence 17284, Application US/10450763  
Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 17284  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIMILAR

LOCATION: (88)..(165)  
OTHER INFORMATION: 100% homologous to Homo sapiens interferon alpha/beta  
OTHER INFORMATION: receptor, accession number X60459, Smith-Waterman Scores=122.  
US-10-450-763-17284  
Query Match 7.3%; Score 98.6; DB 9; Length 579;  
Best Local Similarity 96.2%; Pred. No. 7.7e-15;  
Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CTGCAGGGATCTGCGCGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 60  
DB 62 CTGGTGGGATCTGCGCGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 121  
QY 61 TGCTCGTCCGCGTGGGCGCCATGGGTGTTGTCGCGCAGCCGAGGTG 105  
DB 122 TGCTCGTCCGCGTGGGCGCCATGGGTGTTGTCGCGCAGCCGAGGTG 166  
Search completed: January 18, 2006, 02:01:25  
Job time : 1204 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 17:06:04 ; Search time 874 Seconds  
(without alignments)  
10241.055 Million cell updates/sec

Title: US-10-824-981-1

Perfect score: 1343

Sequence: 1 ctgcaggagctcggcgccg.....ataccttaaatgagggtacc 1343

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1343	100.0	1343	2	AaQ14239 Encodes s
2	1343	100.0	1343	2	AaQ30532 Sequence
3	1343	100.0	1343	2	AaQ49625 Human int
4	1338.2	99.6	1343	2	AaQ86457 IPN-R ext
5	1334	99.3	1755	2	AaQ14240 Encodes c
6	1334	99.3	1755	2	AaQ30533 Sequence
7	1334	99.3	1755	2	AaQ49624 Human int
8	1332.4	99.2	1755	2	AaQ86458 Human IFN
9	1330.8	99.1	2755	11	Adi31792 Human CDN
10	1330.8	99.1	2755	13	Adr66494 Human pro
11	1330.8	99.1	2755	13	Adr66152 Human pro
12	1330.8	99.1	2755	13	Adr83859 Human lym
13	1330.8	99.1	2755	14	Adw86762 Human int
14	1330.8	99.1	2784	2	AaQ11701 Human alp
15	1327.2	98.8	2017	3	Aaf16297 Human pro
c 16	1326	98.7	2278	6	Aas62251 CDNA sequ
17	1326	98.7	2827	13	Acf87579 Human SIR
18	1318.6	98.2	6741	12	AdK23578 Human IFN
19	1313.2	97.8	1512	14	Adv25069 INR1_T11

20	1310.2	97.6	2844	5	AAS81481	Aas81481 DNA encod
21	1308	97.4	1674	14	ADV42429	Adv42429 Human psy
22	1032	76.8	2330	12	ADH22403	Adh22403 Human CDN
23	723.6	53.9	2175	12	ADH22404	Adh22404 Human psy
24	535.4	39.9	1773	14	ADV44169	Adv44169 Human psy
25	251.8	18.7	950	8	ACF64335	AcF64335 Human IFN
26	251.8	18.7	49442	14	AEB96543	Aeb96543 Human IFN
27	182.2	13.6	800	8	ACF64332	AcF64332 Human IFN
28	178.6	13.3	850	8	ACF64333	AcF64333 Human IFN
29	154.8	11.5	700	8	ACF64336	AcF64336 Human IFN
30	127.6	9.5	700	8	ACF64331	AcF64331 Human IFN
31	126	9.4	360	2	AAT73519	Aat73519 Transmemb
32	102.8	7.7	650	8	ACF64334	AcF64334 Human IFN
33	98.6	7.3	579	5	AAS81480	Aas81480 DNA encod
34	98.6	7.3	579	10	ADF59919	Adf59919 Human con
35	98.6	7.3	900	8	ACF64330	AcF64330 Human IFN
36	98.6	7.3	1000	12	ADM79794	Adm79794 Human mic
37	98.6	7.3	1042	10	ACC79180	Acc79180 Human int
38	98.6	7.3	1042	12	ADF49222	Adf49222 Human int
39	98.6	7.3	1044	10	ACC79181	Acc79181 Human int
40	98.6	7.3	1046	10	ACC79182	Acc79182 Human int
41	98.6	7.3	1048	10	ACC79183	Acc79183 Human int
42	98.6	7.3	1050	10	ACC79184	Acc79184 Human int
43	98.6	7.3	1052	10	ACC79185	Acc79185 Human int
44	98.6	7.3	1054	10	ACC79186	Acc79186 Human int
45	98.6	7.3	1056	10	ACC79187	Acc79187 Human int

#### ALIGNMENTS

RESULT 1

AAQ14239  
ID AAQ14239 standard; DNA; 1343 BP.

XX AC AAQ14239;

XX DT 16-JAN-1992 (first entry)

XX DE Encodes soluble interferon-alpha/beta receptor.

XX KW IFN; autoimmune disease; graft rejection; histocompatibility; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 27..1337

XX FT /\*tag= a

XX FT /product= "soluble receptor"

XX PN FR2657881-A.

XX PD 09-AUG-1991.

XX PF 05-FEB-1990; 90FR-00001298.

XX PR 05-FEB-1990; 90FR-00001298.

XX PA (EUBI-) LAB EURO BIOTECHNO.

XX PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey MG;

XX PI Uze G;

XX WPI; 1991-319778/44.

XX P-PSDB; AARI4487.

XX New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.

XX PS Claim 10; Page 45; 52pp; French.

XX CC The protein encoded by this sequence corresponds to the soluble,

CC extracellular portion of the interferon-alpha and/or beta receptor. The  
CC transmembrane and cytoplasmic domains of the native receptor have been  
CC deleted to obtain a soluble, circulating form of the receptor.  
CC Potentially immunogenic epitopes have thus been eliminated. See also  
CC AAQ14240  
XX  
SQ Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1343; DB 2; Length 1343;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTGCAGGGATCTGCGGCGCTCCAGATGATGGTCTCTCCCTGGGCGGACGACCTAG 60  
DB 1 CTGCAGGGATCTGCGGCGCTCCAGATGATGGTCTCTCCCTGGGCGGACGACCTAG 60  
QY 61 TGGTCTGCGCGTGGGCCCATGGGTGTTGTCGAGCGCGGAGGTGGAAAAATCTAAAT 120  
DB 61 TGGTCTGCGCGTGGGCCCATGGGTGTTGTCGAGCGCGGAGGTGGAAAAATCTAAAT 120  
QY 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA 180  
DB 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA 180  
QY 181 GCGATGAGTCTGCGGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240  
DB 181 GCGATGAGTCTGCGGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240  
QY 241 ATTGGAATAAATTGTCGGGTGTCAGAAATATTACTAGTACCAATGCAACTTTTCTTTCAC 300  
DB 241 ATTGGAATAAATTGTCGGGTGTCAGAAATATTACTAGTACCAATGCAACTTTTCTTTCAC 300  
QY 301 TCAAGCTGAATGTTTATGAAGAATAAATTAATGGGTATAAGCAGCAGAAAAAGAACACTT 360  
DB 301 TCAAGCTGAATGTTTATGAAGAATAAATTAATGGGTATAAGCAGCAGAAAAAGAACACTT 360  
QY 361 CTTCATGATGAGGTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
DB 361 CTTCATGATGAGGTGACTCAATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
QY 421 AAGTACATTTAGAAGCTGGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAAG 480  
DB 421 AAGTACATTTAGAAGCTGGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAAG 480  
QY 481 ATAGTGTTATGCGGCTTTGCGGTGTTAAGCTTTACATATAGCTTACTTATCTCGAAA 540  
DB 481 ATAGTGTTATGCGGCTTTGCGGTGTTAAGCTTTACATATAGCTTACTTATCTCGAAA 540  
QY 541 ACTCTTCAGGTGTAGAAAGGATTGAAAATATTTATTCAGACATATAAAATTTATAAAC 600  
DB 541 ACTCTTCAGGTGTAGAAAGGATTGAAAATATTTATTCAGACATATAAAATTTATAAAC 600  
QY 601 TCTCACAGAGACTACTTATTTGCTAAAAGTTAAAGCAGCACTACTTACGTCTATGGAAGA 660  
DB 601 TCTCACAGAGACTACTTATTTGCTAAAAGTTAAAGCAGCACTACTTACGTCTATGGAAGA 660  
QY 661 TTGGTGTCTATAGTCCAGTACATTGTATTAAGCCACAGTTGAAATGAACCTACCTCCAC 720  
DB 661 TTGGTGTCTATAGTCCAGTACATTGTATTAAGCCACAGTTGAAATGAACCTACCTCCAC 720  
QY 721 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTATACAT 780  
DB 721 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTATACAT 780  
QY 781 ATGCAACATGACTTTCAAGTTCAGTGGTCTCCAGCGCTTTTAAAAAGGAATCTCGGAA 840  
DB 781 ATGCAACATGACTTTCAAGTTCAGTGGTCTCCAGCGCTTTTAAAAAGGAATCTCGGAA 840  
QY 841 ACCATTGTATTAATGGAACAAATACCTGACTGTGAATGTCAAACTACCCAGTGTG 900  
DB 841 ACCATTGTATTAATGGAACAAATACCTGACTGTGAATGTCAAACTACCCAGTGTG 900  
QY 901 TCTTTCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960

DB 901 TCTTTCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960  
QY 961 GAAATAACACATCTTTTGGTCTGAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC 1020  
DB 961 GAAATAACACATCTTTTGGTCTGAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC 1020  
QY 1021 TACTTCTCCAGTCTTTTAACATTAGATCCCTTAGTGATTTCATTCATATCTATATCGGTG 1080  
DB 1021 TACTTCTCCAGTCTTTTAACATTAGATCCCTTAGTGATTTCATTCATATCTATATCGGTG 1080  
QY 1081 CTCAAAAACAGTCTGAAAAACACGCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140  
DB 1081 CTCAAAAACAGTCTGAAAAACACGCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140  
QY 1141 TTTTGGGAAAAACACTTCAAAATGCTGAGAAAAAATTCGAGAAAAAACTGATGTTA 1200  
DB 1141 TTTTGGGAAAAACACTTCAAAATGCTGAGAAAAAATTCGAGAAAAAACTGATGTTA 1200  
QY 1201 CAGTTCCTAAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACACCATGG 1260  
DB 1201 CAGTTCCTAAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACACCATGG 1260  
QY 1261 ATCAAAAGCTGAATAAAAAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
DB 1261 ATGAAAGCTGAATAAAAAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
QY 1321 GAAATACCTCTAAATGAGGTACC 1343  
DB 1321 GAAATACCTCTAAATGAGGTACC 1343  
RESULT 2  
AAQ30532  
ID AAQ30532 standard; DNA; 1343 BP.  
XX  
AC AAQ30532;  
XX AC  
DT 25-MAR-2003 (revised)  
DT 31-MAR-1993 (first entry)  
XX  
DE Sequence encoding a soluble form of the interferon (IFN) receptor with a  
DE high affinity for IFN-alpha and -beta.  
XX  
KW Interferon receptor; alpha-interferon; beta-interferon; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 27..1337  
FT /tag= a  
XX  
FN W09218626-A1.  
XX  
PD 29-OCT-1992.  
XX  
PF 17-APR-1991; 91WO-FR000318.  
XX  
PR 17-APR-1991; 91WO-FR000318.  
XX  
(EUBI-) LAB EURO BIOTECHNOLOGIE.  
XX  
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
PI Uze G;  
XX  
DR WPI; 1992-382110/46.  
DR P-PSDB; AAR28495.  
XX  
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
PT useful as immunosuppressants, for treating autoimmune diseases and  
XX transplant rejection.  
PS Claim 10; Fig 1; 58pp; English.

XX DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
 CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
 CC primers and cloned cDNA as template. For example, bacteriophage lambda  
 CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
 CC receptor (AA030533), was incubated with oligos AA030534 and AA030535.  
 CC AA028496 represents the complete receptor. AA028495 lacks the  
 CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
 CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
 CC diseases and graft rejection. They lack the toxic side-effects of known  
 CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX

Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1343; DB 2; Length 1343;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAGGAGCTCGGGGCTCCAGATGATGGTGGTCTCTCGGGCGCAGCCCTAG 60  
 Db 1 CTGCAGGAGCTCGGGGCTCCAGATGATGGTGGTCTCTCGGGCGCAGCCCTAG 60

Qy 61 TGCTCGTCCGCGTGGGCCCATGGGTGTTGTCGGCAGCGCAGGTGGAAAAATCTAAAT 120  
 Db 61 TGCTCGTCCGCGTGGGCCCATGGGTGTTGTCGGCAGCGCAGGTGGAAAAATCTAAAT 120

Qy 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAAACAGGA 180  
 Db 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCGAGGTGGAAACAGGA 180

Qy 181 GCGATGAGTCTGTCGGGAATGACTTTTTCATTCGATTTCAAAAACTGGGATGGATA 240  
 Db 181 GCGATGAGTCTGTCGGGAATGACTTTTTCATTCGATTTCAAAAACTGGGATGGATA 240

Qy 241 ATTGATTAATAATTTCTGGGTGTCAGATATATCTAGTACCAATGCAACTTTCTTCAC 300  
 Db 241 ATTGATTAATAATTTCTGGGTGTCAGATATATCTAGTACCAATGCAACTTTCTTCAC 300

Qy 301 TCAAGCTCAATGTTTATCAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 360  
 Db 301 TCAAGCTCAATGTTTATCAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 360

Qy 361 CTTTCATGTTATGAGGTGCTGACTCATTTACACCAATTTGCGAAAGCTCAGATTGCTCCAG 420  
 Db 361 CTTTCATGTTATGAGGTGCTGACTCATTTACACCAATTTGCGAAAGCTCAGATTGCTCCAG 420

Qy 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTATGATACATCTCTCTCGGAACAAAG 480  
 Db 421 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTATGATACATCTCTCTCGGAACAAAG 480

Qy 481 ATAGTGTATGTTGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTACTTCTGGAATA 540  
 Db 481 ATAGTGTATGTTGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTACTTCTGGAATA 540

Qy 541 ACTCTTCAGGTGTAGAAGAAAGATTGAAAATATTTATTTCCAGACATAAAATTTATAAC 600  
 Db 541 ACTCTTCAGGTGTAGAAGAAAGATTGAAAATATTTATTTCCAGACATAAAATTTATAAC 600

Qy 601 TCTCACCAGAGACTACTTATTGCTCTAAAGTTAAAGCAGCACTACTTACGTCATGAAAA 660  
 Db 601 TCTCACCAGAGACTACTTATTGCTCTAAAGTTAAAGCAGCACTACTTACGTCATGAAAA 660

Qy 661 TTGGTGTCTATAGTCCAGTACATTTCTATATAAGACACACAGTTGAAAATGAACTTCCAC 720  
 Db 661 TTGGTGTCTATAGTCCAGTACATTTCTATATAAGACACACAGTTGAAAATGAACTTCCAC 720

Qy 721 CAGAAATATAGAAGTCCAGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780  
 Db 721 CAGAAATATAGAAGTCCAGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780

Qy 781 ATGCAAAACATGACCTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGAA 840  
 Db 781 ATGCAAAACATGACCTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGAA 840

Db 781 ATGCAAAACATGACCTTCAAGTTTCAGTGGCTCCAGCGCTTTTAAAAAGGAATCTCGAA 840  
 Qy 841 ACCATTTGTATAAATGAAACAAATACCTGCTGTGAAAAATGTCAAACTACCCAGTGTG 900  
 Db 841 ACCATTTGTATAAATGAAACAAATACCTGCTGTGAAAAATGTCAAACTACCCAGTGTG 900  
 Qy 901 TCTTCTCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGGGTCAAGCACTCTGATG 960  
 Db 901 TCTTCTCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGGGTCAAGCACTCTGATG 960  
 Qy 961 GAAATAACACATCTTTTGTGCTGAAGAGATAAAGTTTGTATCTGAAATACAAGCTTTCC 1020  
 Db 961 GAAATAACACATCTTTTGTGCTGAAGAGATAAAGTTTGTATCTGAAATACAAGCTTTCC 1020

Qy 1021 TACTTCTCCAGCTTTTAAACATTTAGATCCCTTAGTGAATTCATTCATATCTATATCGTG 1080  
 Db 1021 TACTTCTCCAGCTTTTAAACATTTAGATCCCTTAGTGAATTCATTCATATCTATATCGTG 1080

Qy 1081 CTCCAAAACAGTCTGGAACACGCTCTGTGATCCAGGATTTCCACTGATTTATGAAATTA 1140  
 Db 1081 CTCCAAAACAGTCTGGAACACGCTCTGTGATCCAGGATTTCCACTGATTTATGAAATTA 1140

Qy 1141 TTTTTCGGAAAAACACTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
 Db 1141 TTTTTCGGAAAAACACTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200

Qy 1201 CAGTTCCTAAATTTGAAACCACTGATGATATTTGTGTAAGCCAGAGCAACACCATGG 1260  
 Db 1201 CAGTTCCTAAATTTGAAACCACTGATGATATTTGTGTAAGCCAGAGCAACACCATGG 1260

Qy 1261 ATGAAAAGCTCAATTAAGAGCAGTGTGTTTAGTGAGCGTGTATGTGAGAAAAACAAACCAG 1320  
 Db 1261 ATGAAAAGCTCAATTAAGAGCAGTGTGTTTAGTGAGCGTGTATGTGAGAAAAACAAACCAG 1320

Qy 1321 GAAATACCTCTAAATGAGGTACC 1343  
 Db 1321 GAAATACCTCTAAATGAGGTACC 1343

RESULT 3  
 AA049625  
 ID AA049625 standard; DNA; 1343 BP.  
 XX AA049625;  
 AC AC  
 XX 25-MAR-2003 (revised)  
 DT 20-APR-1994 (first entry)  
 XX Human interferon receptor extracellular domain coding sequence.  
 DE  
 XX IFN-R; extracellular domain; monoclonal antibody; viral infection;  
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;  
 KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;  
 KW immunodeficiency; measles virus; interferon-alpha-beta; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 CDS 27..1337  
 FT /\*tag= a  
 FT /note= "encodes extra cellular domain of IFN-R"  
 XX  
 PN EP563487-A1.  
 XX  
 XX 06-OCT-1993.  
 XX  
 XX 31-MAR-1992; 92EP-00400902.  
 XX  
 XX 31-MAR-1992; 92EP-00400902.  
 XX  
 XX (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 XX Benoit P, Meyer F, Maguire D, Plavec I, Tovey MG;





DR WPI; 1991-319776/44.  
XX P-PSDB; AAR14488.  
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
PT used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
PT anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
XX  
PS Disclosure; Page 47; 52pp; French.  
XX  
XX The protein encoded by this sequence corresponds to the complete  
CC interferon-alpha and/or beta receptor. The invention covers derivatives  
CC of the receptor obtained by deleting the transmembrane and cytoplasmic  
CC domains of the native receptor or by substitution. See also AAQ14239  
XX  
SQ Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T; 0 U; 0 Other;  
  
Query Match 99.38; Score 1334; DB 2; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CTG CAGGAGATCTGGCGGGCTCCAGATGATGGTGCCTCTGGGGCGGACGACCCCTAG 60  
DB 1 CTG CAGGAGATCTGGCGGGCTCCAGATGATGGTGCCTCTGGGGCGGACGACCCCTAG 60  
  
QY 61 TGC TCGTCCGCGTGGGCCCATGGTGTTCG CAGCGCCGAGGTGGAAAAATCTAAAT 120  
DB 61 TGC TCGTCCGCGTGGGCCCATGGTGTTCG CAGCGCCGAGGTGGAAAAATCTAAAT 120  
  
QY 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGAACAGGA 180  
DB 121 CTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGAACAGGA 180  
  
QY 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGGATGGATA 240  
DB 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAACCTGGGATGGATA 240  
  
QY 241 ATTGGATAAAATTTGTCTGGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTCAC 300  
DB 241 ATTGGATAAAATTTGTCTGGGTGTCAGAAATATTAAGTACCAATGCAACTTTTCTTCAC 300  
  
QY 301 TCAAGCTGAATGTTATGAAGAAATTAATTCGTTATAGAGCGAAAAAGAAACACTT 360  
DB 301 TCAAGCTGAATGTTATGAAGAAATTAATTCGTTATAGAGCGAAAAAGAAACACTT 360  
  
QY 361 CTTCATGATGAGTGTGACTCATTTACACATTTCCGAAAGCTCAGATTGGTCTCCAG 420  
DB 361 CTTCATGATGAGTGTGACTCATTTACACATTTCCGAAAGCTCAGATTGGTCTCCAG 420  
  
QY 421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 480  
DB 421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTGGAAACAAAG 480  
  
QY 481 ATAGTGTTATGCGGCTTTGGATGGTTTAACTTTACATATAGTCTTACTTCGAAAA 540  
DB 481 ATAGTGTTATGCGGCTTTGGATGGTTTAACTTTACATATAGTCTTACTTCGAAAA 540  
  
QY 541 ACTCTTCAGGTGTGAAGAAAGGATGAAATATTTATTCAGACATATAAATTTATAAAC 600  
DB 541 ACTCTTCAGGTGTGAAGAAAGGATGAAATATTTATTCAGACATATAAATTTATAAAC 600  
  
QY 601 TCTCACCAGAGACTACTTATTTGTCTAAAAGTTAAAGCAGCAGCTACTTACGTATGAAAAA 660  
DB 601 TCTCACCAGAGACTACTTATTTGTCTAAAAGTTAAAGCAGCAGCTACTTACGTATGAAAAA 660  
  
QY 661 TTGGTGTCTATAGTCCAGTACATTTGTATAAGACCAAGTTGAAATGAATCTACCTCCAC 720  
DB 661 TTGGTGTCTATAGTCCAGTACATTTGTATAAGACCAAGTTGAAATGAATCTACCTCCAC 720  
  
QY 721 CAGAAATATAGAGTGCAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTTATACAT 780  
DB 721 CAGAAATATAGAGTGCAGTGTCCAAATCAGAACTATGTTCTTAATGGGATTTATACAT 780  
  
QY 781 ATGCAAAACATGACCTTTTCAAGTTCAGTGGCTCCACGCCCTTTTAAAAAGGAATCTCGAA 840

781 ATGCAAAACATGACCTTTTCAAGTTCAGTGGCTCCACGCCCTTTTAAAAAGGAATCTCGAA 840  
841 ACCATTGTGTATAAATGGAACAAATACCTGACTGTGAAAATGTCAAAATCTACCCAGTGTG 900  
841 ACCATTGTGTATAAATGGAACAAATACCTGACTGTGAAAATGTCAAAATCTACCCAGTGTG 900  
901 TCTTTCTCTCAAAACGTTTTTCCAAAAAGGAATTTTACCTTCTCCGCGTACAGCATCTGATG 960  
901 TCTTTCTCTCAAAACGTTTTTCCAAAAAGGAATTTTACCTTCTCCGCGTACAGCATCTGATG 960  
961 GAAATTAACATCTTTTGGTCTGAAAGATAAAGTTTGAATCTGAAATCTGAAATCTGAAATCTTCC 1020  
961 GAAATTAACATCTTTTGGTCTGAAAGATAAAGTTTGAATCTGAAATCTGAAATCTGAAATCTTCC 1020  
1021 TACTTCTCTCAGTCTTTTAAACATTTAGATCCCTTAGTGTGATTCATTCATCTATATCGGTG 1080  
1021 TACTTCTCTCAGTCTTTTAAACATTTAGATCCCTTAGTGTGATTCATTCATCTATATCGGTG 1080  
1081 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA 1140  
1081 CTCAAAAACAGTCTGAAAAACAGCCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA 1140  
1141 TTTTGGGAAAAACACTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
1141 TTTTGGGAAAAACACTTCAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGGAAGCCAGCACACCATGG 1260  
1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGGAAGCCAGCACACCATGG 1260  
1261 ATGAAAGCTGAATTAAGCAGTGTGTTTGTAGTGCCTGTATGTGAGAAAAACAAAAACCAG 1320  
1261 ATGAAAGCTGAATTAAGCAGTGTGTTTGTAGTGCCTGTATGTGAGAAAAACAAAAACCAG 1320  
1321 GAAATACCTCTAAA 1334  
1321 GAAATACCTCTAAA 1334  
  
RESULT 6  
AAQ30533  
ID AAQ30533 standard; DNA; 1755 BP.  
XX  
AC AAQ30533;  
XX  
XX 25-MAR-2003 (revised)  
DT 31-MAR-1993 (first entry)  
XX  
DE Sequence encoding a soluble form of the interferon (IFN) receptor with a  
DE high affinity for IFN-alpha and -beta.  
XX  
XX Interferon receptor; alpha-interferon; beta-interferon; ss.  
XX  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
CDS 27..1700  
FT /\*tag= a  
XX  
XX WO9218626-A1.  
PN  
XX  
XX 29-OCT-1992.  
XX  
PF 17-APR-1991; 91WO-FR000318.  
XX  
XX 17-APR-1991; 91WO-FR000318.  
XX  
XX (EUBI-) LAB EURO BIOTECHNOLOGIE.  
PA  
XX Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
PI Uze G;  
XX

DR	WFI; 1992-382110/46.
XX	P-PSDB; AAR28496.
DR	
XX	
PT	Water soluble polypeptide(s) strongly bind interferon(α) alpha and beta -
PT	useful as immunosuppressants, for treating auto-immune diseases and
PT	transplant rejection.
XX	
PS	Claim 10; Fig 2; 58pp; English.
CC	DNA encoding the water-soluble polypeptide with a high affinity for IFN-
CC	alpha and -beta is isolated by PCR, using appropriate oligonucleotides as
CC	primers and cloned cDNA as template. For example, bacteriophage lambda
CC	ZAP, containing the entire coding sequence of the IFN-alpha and -beta
CC	receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.
CC	AAAR28496 represents the complete receptor. AAR28495 lacks the
CC	transmembrane and cytoplasmic domains. Both forms bind IFN in the same
CC	way as antibodies so are immunosuppressants e.g. for treating autoimmune
CC	diseases and graft rejection. They lack the toxic side-effects of known
CC	immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct
CC	PN field.)
XX	
SQ	Sequence 1755 BP; 593 A; 325 C; 333 G; 504 T; 0 U; 0 Other;
	Query Match . 99.3%; Score 1334; DB 2; Length 1755;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTCAGGGATCTCGGCGGTCCACAGATGATGTCCTCCTCGGCGGCAGACCCTAG 60
DB	1 CTCAGGGATCTCGGCGGTCCACAGATGATGTCCTCCTCGGCGGCAGACCCTAG 60
QY	61 TGCTCGTCCGCGTGCCGCCATGGTGTTCGCCAGCCGCGAGTGGAAAAAATCTAAAAT 120
DB	61 TGCTCGTCCGCGTGCCGCCATGGTGTTCGCCAGCCGCGAGTGGAAAAAATCTAAAAT 120
QY	121 CTCTCAAAAGTAGAGTGCATCATATAGATGACAATTATCTCTGAGGTGGAAACAGGA 180
DB	121 CTCTCAAAAGTAGAGTGCATCATATAGATGACAATTATCTCTGAGGTGGAAACAGGA 180
QY	181 GCATGAGTCTGCGGGAATGTACTTTTTCATGATTTATCAAAAAAATCGGATGGATA 240
DB	181 GCATGAGTCTGCGGGAATGTACTTTTTCATGATTTATCAAAAAAATCGGATGGATA 240
QY	241 ATTGGATAAAATGTCTGGGTGTGAGAATATTACTAGTACCAAATGCAACTTTTCTCAC 300
DB	241 ATTGGATAAAATGTCTGGGTGTGAGAATATTACTAGTACCAAATGCAACTTTTCTCAC 300
QY	301 TCAAGTGAATGTTTTATGAAGAAATTAATTCGTTATAGACAGAAAAAAGAACACTT 360
DB	301 TCAAGTGAATGTTTTATGAAGAAATTAATTCGTTATAGACAGAAAAAAGAACACTT 360
QY	361 CTTTCATGGTATGAGTGTGATCAATTTACACCAATTTTCGCAAGCTCAGATTGGTCTCCAG 420
DB	361 CTTTCATGGTATGAGTGTGATCAATTTACACCAATTTTCGCAAGCTCAGATTGGTCTCCAG 420
QY	421 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGAAACAAAG 480
DB	421 AAGTACATTTAGAAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGAAACAAAG 480
QY	481 ATAGTGTATGTCGGCTTTGGATGGTTAAGCTTTTACATATAGCTTACTTATCTCGAAAA 540
DB	481 ATAGTGTATGTCGGCTTTGGATGGTTAAGCTTTTACATATAGCTTACTTATCTCGAAAA 540
QY	541 ACTCTTCAGGTGTAGAAAGAGGATTAATAATTTATTTCCAGACATAAAATTTATAAC 600
DB	541 ACTCTTCAGGTGTAGAAAGAGGATTAATAATTTATTTCCAGACATAAAATTTATAAC 600
QY	601 TCTCACCAGAGACTACTTATTTCTAAAAGTTTAAAGCAGCACTACTTACGTCATGAAAA 660
DB	601 TCTCACCAGAGACTACTTATTTCTAAAAGTTTAAAGCAGCACTACTTACGTCATGAAAA 660
QY	661 TTGGTGTCTATAGTCCAGTACATTGTATTAAGACACACAGTTGAAAAATGAACCTCCAC 720

Db	661	TTGGTGTCTATAGTCCAGTACATTGTATTAAGACACACAGTTGAAAAATGAACCTCCAC	720
Qy	721	CAGAAAAATATAGAAGTCAGTGTCCAAAAATCAGAACTATCTTCTTAAATGGGATTATACAT	780
Db	721	CAGAAAAATATAGAAGTCAGTGTCCAAAAATCAGAACTATCTTCTTAAATGGGATTATACAT	780
Qy	781	ATGCAAAACATGACCTTTTCAAGTTTCAGTGGCTCCAGCCCTTTTAAAGGAATCTCTGGA	840
Db	781	ATGCAAAACATGACCTTTTCAAGTTTCAGTGGCTCCAGCCCTTTTAAAGGAATCTCTGGA	840
Qy	841	ACCATTTGTATTAATCGAAACAAATACCTGACTGTGAAAAATGTCAAAATCTACCCAGTGTG	900
Db	841	ACCATTTGTATTAATCGAAACAAATACCTGACTGTGAAAAATGTCAAAATCTACCCAGTGTG	900
Qy	901	TCTTCTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACCAAGCATCTGATG	960
Db	901	TCTTCTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACCAAGCATCTGATG	960
Qy	961	GAAATTAACACATCTTTTGGTCTGAAAGAGATAAAGTTTGAATCTGAAATPACAAGCTTTCC	1020
Db	961	GAAATTAACACATCTTTTGGTCTGAAAGAGATAAAGTTTGAATCTGAAATPACAAGCTTTCC	1020
Qy	1021	TACTCTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG	1080
Db	1021	TACTCTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG	1080
Qy	1081	CTCAAAACAGTCTGAAAAACAGCCCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA	1140
Db	1081	CTCAAAACAGTCTGAAAAACAGCCCTGTGATCCAGGATTTATCCACTGATTTATGAAATTA	1140
Qy	1141	TTTTTTGGGAAAAACATCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAATCTGATG	1200
Db	1141	TTTTTTGGGAAAAACATCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAATCTGATG	1200
Qy	1201	CAGTCTCTAAATTTGAAACCACTGATATTTGTGTAAGCCAGACACACACCATGG	1260
Db	1201	CAGTCTCTAAATTTGAAACCACTGATATTTGTGTAAGCCAGACACACACCATGG	1260
Qy	1261	ATGAAAGCTGTAATAAAGCAGTGTGTTTGTAGTGAAGCTGTATGTGAGAAAAAACAACAC	1320
Db	1261	ATGAAAGCTGTAATAAAGCAGTGTGTTTGTAGTGAAGCTGTATGTGAGAAAAAACAACAC	1320
Qy	1321	GAAATACCTCTTAA 1334	
Db	1321	GAAATACCTCTTAA 1334	
	RESULT 7		
	AAQ49624		
ID	AAQ49624	standard; DNA; 1755 BP.	
XX	AAQ49624;		
AC	AAQ49624;		
DT	25-MAR-2003 (revised)		
DT	20-APR-1994 (first entry)		
DE	Human interferon receptor coding sequence.		
KW	IFN-R; extracellular domain; monoclonal antibody; viral infection;		
KW	cell proliferation; allograft rejection; systemic lupus erythematosus;		
KW	psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;		
KW	immunodeficiency; measles virus; interferon-alpha-beta; ss.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FH	CDS	27..1700	
FT	/tag= a		
FT	/product= "hIFN-R"		
FT	/note= "antibodies are pref. raised to soluble forms of		
FT	the receptor, i.e. to the extracellular domain"		
XX	EP563487-A1.		







[illegible]

AD66494	AD66494 standard; DNA; 2755 BP.	Query Match	99.1%; Score 1330.8; DB 13; Length 2755;
ID	AD66494	Best Local Similarity	99.9%; Pred. No. 0;
XX	AC	Matches 1332; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
XX	AC		
XX	02-DEC-2004 (first entry)		
XX	DE	Human prostatic carcinoma derived DNA SEQ ID 6 #3.	
XX	DE		
XX	KW	human; cytostatic; diagnosis; prostatic cancer;	
XX	KW	differential expression analysis; ds.	
XX	XX		
XX	OS	Homo sapiens.	
XX	XX		
XX	FN	WO2004076614-A2.	
XX	XX		
XX	PD	10-SEP-2004.	
XX	XX		
XX	PF	22-FEB-2004; 2004WO-DE000433.	
XX	XX		
XX	PR	27-FEB-2003; 2003DE-01009985.	
XX	PR	14-MAY-2003; 2003DE-01022134.	
XX	XX		
XX	PA	(HINZ/) HINZMANN B.	
XX	PA	(DAHL/) DAHL E.	
XX	PA	(ROSE/) ROSENTHAL A.	
XX	PA	(HERM/) HERMANN K.	
XX	PA	(PILA/) PILARSKY C.	
XX	XX		
XX	PI	Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;	
XX	PI	Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;	
XX	PI	Xinzhong L, Staub E;	
XX	XX		
XX	DR	WPI; 2004-653386/63.	
XX	XX		
XX	PT	New nucleic acids, and encoded proteins, from prostatic cancer tissue,	
XX	PT	useful for diagnosis, treatment and in screening for specific binding	
XX	PT	agents.	
XX	XX		
XX	XX	Claim 1; Page 1087; 1607pp; German.	
XX	PS		
XX	CC	This invention describes novel cytostatic polynucleotide and polypeptide	
XX	CC	sequences which can be used in a method for diagnosing prostatic cancer	
XX	CC	or the risk of developing prostatic cancer. Diagnosis is based on	
XX	CC	determining over transcription or over expression of the sequences in	
XX	CC	prostatic tissue. Screening for inhibitors of the sequences or detection	
XX	CC	substances involves a binding assay, any compounds that bind are	
XX	CC	selected, optionally after deconvolution of mixtures. Detection of a	
XX	CC	predetermined minimum level of the reporter indicates the presence of	
XX	CC	tumour cells. Inhibitors can be chosen from antisense oligonucleotides,	
XX	CC	short-interfering RNA or ribozymes; an organic molecule of molecular	
XX	CC	weight below 5000, preferably 300, that binds to the polypeptide; an	
XX	CC	aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the	
XX	CC	polypeptide, preferably humanised or human; an anti-idiotypic, non-human	
XX	CC	(monoclonal) antibody directed against Ab or any of the above derivatised	
XX	CC	with a reporter group, cell toxin, immunostimulatory molecules and/or	
XX	CC	radioisotope. The polynucleotides are identified in human prostatic	
XX	CC	cancer by differential expression analysis, using DNA microarrays,	
XX	CC	between normal and tumorous tissues, with (over)expression being detected	
XX	CC	by quantitative PCR. Analysis of prostatic cancer samples showed that	
XX	CC	CD24 was upregulated in many of them. Sections of tissue, isolated from	
XX	CC	prostatic cancer patients, or subjects at risk, were incubated	
XX	CC	sequentially with anti-human CD4 murine monoclonal antibodies;	
XX	CC	biotinylated second antibody; streptavidin-conjugated horseradish	
XX	CC	peroxidase and then diaminobenzidine as colour former (brown). The	
XX	CC	samples were counterstained with hemalum (blue). Malignant cells stained	
XX	CC	strongly but non-malignant cells only weakly. In 15 of 63 samples of	
XX	CC	adenocarcinoma, membrane and cytoplasmic staining was very strong, and	
XX	CC	lymph node metastases were also stained. AD65805-AD66954 represent the	
XX	CC	polynucleotide and polypeptide sequences used in the method of the	
XX	CC	invention.	
XX	XX		
XX	XX	Sequence 2755 BP; 867 A; 553 C; 578 G; 757 T; 0 U; 0 Other;	

Qy 1021 TACTTCTCCAGCTTTTAAACATTAGATCCCTTAGTGATTCAATCCATATCTATATCGGTG 1080  
Db TACTTCTCCAGCTTTTAAACATTAGATCCCTTAGTGATTCAATCCATATCTATATCGGTG 1132  
Qy 1081 CTCCTCAACAGCTCTGGAACACGCGCTGTGATCCAGGATTATCCACTGATTTATGAATTA 1140  
Db TCTCAAAACAGCTCTGGAACACGCGCTGTGATCCAGGATTATCCACTGATTTATGAATTA 1192  
Qy 1141 TTTTTCGGGAAACACATTTCAAAATGCTGAGAGAAAAATATTCGAGAAAAAACTGATGTTA 1200  
Db TTTTTCGGGAAACACATTTCAAAATGCTGAGAGAAAAATATTCGAGAAAAAACTGATGTTA 1252  
Qy 1201 CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACCATGG 1260  
Db CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACCATGG 1312  
Qy 1261 ATGAAAAGCTGAATAAAGCAGTGTGTTTTTGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320  
Db ATGAAAAGCTGAATAAAGCAGTGTGTTTTTGTGACGCTGTATGTGAGAAAAACAAACCCAG 1372  
Qy 1321 GAAATACCTCTAAA 1334  
Db GAAATACCTCTAAA 1386

RESULT 11

ADR66152  
ID ADR66152 standard; DNA; 2755 BP.

AC ADR66152;

XX 02-DEC-2004 (first entry)

XX Human prostatic carcinoma derived DNA SEQ ID 6 #2.

XX human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis; ds.

XX Homo sapiens.

XX WO2004076614-A2.

XX 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.

PR 14-MAY-2003; 2003DE-01022134.

XX (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.

PA (PILA/) PILARSKY C.

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;

PI Schmitt A, Beckmann G, Bruemendorf T, Kinneemann H, Roepcke S;

PI Xinzhang L, Staub E;

XX WPI; 2004-653386/63.

DR New nucleic acids, and encoded proteins, from prostatic cancer tissue,

XX useful for diagnosis, treatment and in screening for specific binding

PT agents.

PT Claim 1; Page 481; 1607pp; German.

PS This invention describes novel cytostatic polynucleotide and polypeptide

XX sequences which can be used in a method for diagnosing prostatic cancer

CC or the risk of developing prostatic cancer. Diagnosis is based on

CC determining over transcription or over expression of the sequences in

CC prostatic tissue. Screening for inhibitors of the sequences or detection

XX substances involves a binding assay, any compounds that bind are

CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.  
XX  
SQ Sequence 2755 BP; 867 A; 553 C; 578 G; 757 T; 0 U; 0 Other;

Query Match 99.1%; Score 1330.8; DB 13; Length 2755;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGACGGGATCTGCGCGGCTCCAGATGATGTCCTCTCTGGCGGACGACCCCTAG 60  
Db TCTGCGGATCTGCGCGGCTCCAGATGATGTCCTCTCTGGCGGACGACCCCTAG 112  
Qy 61 TGCTCTGCGCGGTCGCGGCTCCAGATGATGTCCTCTCTGGCGGACGACCCCTAG 120  
Db TGCTCTGCGCGGTCGCGGCTCCAGATGATGTCCTCTCTGGCGGACGACCCCTAG 172  
Qy 121 CTCCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTATCTCTGAGGTGGACAGGA 180  
Db CTCCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTATCTCTGAGGTGGACAGGA 232  
Qy 181 GCGATGAGTCTGTCGGGAATGTGACATTTTCATTCGATTATCAAAAACCTGGGATGGATA 240  
Db GCGATGAGTCTGTCGGGAATGTGACATTTTCATTCGATTATCAAAAACCTGGGATGGATA 292  
Qy 241 ATTGGATAAAATTTGTCGGGTGTCAGAAATATTAATACTAGTACCAATGCAACTTTTCTTCAC 300  
Db ATTGGATAAAATTTGTCGGGTGTCAGAAATATTAATACTAGTACCAATGCAACTTTTCTTCAC 352  
Qy 301 TCAAGCTGGAATGTTATGAAGAAATTAATTTGCGTATAGAGCAGAGAAAGAAACACTT 360  
Db TCAAGCTGGAATGTTATGAAGAAATTAATTTGCGTATAGAGCAGAGAAAGAAACACTT 412  
Qy 361 CTTTCATGGTATGAGGTTGACTCATTTACACCATTTTCGCAAGCTCAGATTGGTCTCCAG 420  
Db CTTTCATGGTATGAGGTTGACTCATTTACACCATTTTCGCAAGCTCAGATTGGTCTCCAG 472  
Qy 421 AAGTACATTTAGAAAGCTGAAGCAATAGTGTATACATCTCTCTCTGGAAACAAAAG 480  
Db AAGTACATTTAGAAAGCTGAAGCAATAGTGTATACATCTCTCTCTGGAAACAAAAG 532  
Qy 481 ATAGTGTATGCGGCTTTGGATGGTTAAGCTTTTACATATAGTACTTATCTCGGAAA 540  
Db ATAGTGTATGCGGCTTTGGATGGTTAAGCTTTTACATATAGTACTTATCTCGGAAA 592  
Qy 541 ACTCTTTCAAGTGTAGAAAGAAAGGATTTGAAAATATTTATTCAGACATATAATTTATAAAC 600  
Db ACTCTTTCAAGTGTAGAAAGAAAGGATTTGAAAATATTTATTCAGACATATAATTTATAAAC 652  
Qy 601 TCTCACGAGACTACTTATTTGCTAAAAGTTAAAGCAGCAGTACTTACGTCATGGAAA 660  
Db TCTCACGAGACTACTTATTTGCTAAAAGTTAAAGCAGCAGTACTTACGTCATGGAAA



Db 593 ACTCTTCAGGTGTAGAGAGAAGGATTGAAAATATTTATTCAGACATAAAAAATTTATAAAC 652  
Qy 601 TCTCACCAGAGACTACTTATTGTCTAAAGTTAAAGCAGCAGCTACTTACGTCATGGAAA 660  
Db 653 TCTCACCAGAGACTACTTATTGTCTAAAGTTAAAGCAGCAGCTACTTACGTCATGGAAA 712  
Qy 661 TTGTGTCTTAGTCCAGTACATTGTATAAAGCACAGCTTTGAAAATGAACTACCTCCAC 720  
Db 713 TTGTGTCTTAGTCCAGTACATTGTATAAAGCACAGCTTTGAAAATGAACTACCTCCAC 772  
Qy 721 CAGAAAATATAGAGTCAGTGTCCAAAATCAGAACTATGTCTTAAATGGGATATACAT 780  
Db 773 CAGAAAATATAGAGTCAGTGTCCAAAATCAGAACTATGTCTTAAATGGGATATACAT 832  
Qy 781 ATGCAACATGACCTTTCAAGTTCAGTGTCCAGCGCTTTTAAAGAGAAATCCTGGAA 840  
Db 833 ATGCAACATGACCTTTCAAGTTCAGTGTCCAGCGCTTTTAAAGAGAAATCCTGGAA 892  
Qy 841 ACCATTTGTATAATGAAAACAAATACCTGACTGTGAAAATGTCAAACTACCCAGTGTG 900  
Db 893 ACCATTTGTATAATGAAAACAAATACCTGACTGTGAAAATGTCAAACTACCCAGTGTG 952  
Qy 901 TCTTCTCCTCAAAAGCTTTTCAAAAAGAAATTTACCTTCTCCGCGTACAAGCATCTGATG 960  
Db 953 TCTTCTCCTCAAAAGCTTTTCAAAAAGAAATTTACCTTCTCCGCGTACAAGCATCTGATG 1012  
Qy 961 GAAATAACATCTCTTTTGGTCTGAAGAGATAAGTTTGATCTGAAATACAGCTTTCC 1020  
Db 1013 GAAATAACATCTCTTTTGGTCTGAAGAGATAAGTTTGATCTGAAATACAGCTTTCC 1072  
Qy 1021 TACTTCTCCAGTCTTAAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTG 1080  
Db 1073 TACTTCTCCAGTCTTAAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTG 1132  
Qy 1081 CTCAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTATCCATGATTTATCAAAATTA 1140  
Db 1133 CTCAAAACAGTCTGGAACACACGCTGTGATCCAGGATTTATCCATGATTTATCAAAATTA 1192  
Qy 1141 TTTTGGGAAAACACTTCAATAGCTCAGAGAAAATATTCGAGAAAACACTGATGTTA 1200  
Db 1193 TTTTGGGAAAACACTTCAATAGCTCAGAGAAAATATTCGAGAAAACACTGATGTTA 1252  
Qy 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1260  
Db 1253 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1312  
Qy 1261 ATGAAAAGCTGAATATAAAGCAGTGTTTTATGTGACGCTGTATGTGAGAAAACAAAACCCAG 1320  
Db 1313 ATGAAAAGCTGAATATAAAGCAGTGTTTTATGTGACGCTGTATGTGAGAAAACAAAACCCAG 1372  
Qy 1321 GAAATACCTCTAAA 1334  
Db 1373 GAAATACCTCTAAA 1386

RESULT 13  
ID ADW86762 standard; DNA; 2755 BP.  
XX AC ADW86762;  
XX AC (first entry)  
DT 07-APR-2005  
XX Human interferon receptor I encoding DNA.  
DE protein interaction; fusion protein; ss; PCR; primer.  
XX Homo sapiens.  
XX OS  
XX PN W02005007822-A2.  
XX PD 27-JAN-2005.

XX PF 09-JUL-2004; 2004WO-US021887.  
XX PR 09-JUL-2003; 2003US-0485968P.  
XX PR 15-OCT-2003; 2003US-0511918P.  
XX PR 27-APR-2004; 2004US-0566113P.  
XX PA (SENT-) SENTIGEN BIOSCIENCES INC.  
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX PI Lee KJ, Axel R, Strapps W, Barnea G;  
XX WPI; 2005-102091/11.  
XX DR Determining protein/protein interaction modulator comprises contacting  
XX PT the compound to a cell transformed or transfected with G-protein coupled  
XX PT receptor and arrestin.  
XX PS Example 24; SEQ ID NO 81; 133pp; English.  
XX CC The invention relates to a novel method for determining if a test-  
XX CC compound modulates a specific protein/protein interaction or protein  
XX CC interactions of interest. The method comprises contacting the compound to  
XX CC a cell or samples of cells, each of which has been transformed or  
XX CC transfected with a nucleic acid molecule. The invention further  
XX CC comprises: a recombinant cell, transformed or transfected with any of the  
XX CC nucleic acid molecules; an isolated nucleic acid molecule comprising, in  
XX CC 5' to 3' order, any of the nucleotide sequences described; an expression  
XX CC vector comprising the isolated nucleic acid molecule of above, operably  
XX CC linked to a promoter; a fusion protein produced by expression of the  
XX CC isolated nucleic acid molecule of above; and a test kit, useful for  
XX CC determining if a test compound modulates a specific protein/protein  
XX CC interaction of interest. The methods, nucleic acid molecules, and kit are  
XX CC useful for determining if a test-compound modulates a specific  
XX CC protein/protein interaction or protein interactions of interest. This  
XX CC polynucleotide sequence represents the human interferon receptor I  
XX CC encoding DNA used in the method of the invention.  
XX SQ Sequence 2755 BP; 867 A; 553 C; 578 G; 757 T; 0 U; 0 Other;

Query Match 99.1%; Score 1330.8; DB 14; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTGACGGGATCTCGGGGGCTCCACATGATGGTCTCTCTGGGGGCGACGCCCTAG 60  
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Qy 121 CTCCTCAAAAAGTAGAGGTGCGACATCATAGATGACAACTTTATCTGAGGTGGAACAGGA 180  
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Qy 181 GCATGAGTCTGTGCGGAATGTGACATTTTTCATTCGATTTATCAAAAACCTGGGATGATA 240  
Db 233 GCGATGAGTCTGTGCGGAATGTGACATTTTTCATTCGATTTATCAAAAACCTGGGATGATA 292  
Qy 241 ATTGGATAAAATTTGCTGGGTGTGAGAAATTTAAATTTGGGTATAGAGCAGAAAAAACAACCTT 300  
Db 293 ATTGGATAAAATTTGCTGGGTGTGAGAAATTTAAATTTGGGTATAGAGCAGAAAAAACAACCTT 352  
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Qy 841 ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG 900  
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Qy 1321 GAAATACCTCTAAA 1334  
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RESULT 14

AAQ11701 ID AAQ11701 standard; DNA; 2784 BP.

XX AC AAQ11701;

XX AC AAQ11701;

DT 18-JUL-1991 (first entry)

XX DE Human alpha-interferon receptor protein encoding sequence.

XX Human alpha IFN; IFN agonists; antiviral; anti tumour agent;  
KW drug targeting; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 79..1752  
FT /tag= a  
FT /product= "human alpha IFN"  
FT sig\_peptide 79..159  
FT /tag= b  
FT /product= "signal peptide"  
FT misc\_rna 226..234  
FT /tag= c  
FT misc\_rna 250..258  
FT /tag= d  
FT misc\_rna 319..327  
FT /tag= e  
FT misc\_rna 340..348  
FT /tag= f  
FT misc\_rna 406..414  
FT /tag= g  
FT misc\_rna 592..600  
FT /tag= h  
FT misc\_rna 838..847  
FT /tag= i  
FT misc\_rna 1015..1023  
FT /tag= j  
FT misc\_rna 1018..1026  
FT /tag= k  
FT misc\_rna 1204..1212  
FT /tag= l  
FT misc\_rna 1324..1332  
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FT /tag= o  
FT misc\_rna 1630..1638  
FT /tag= p  
FT misc\_rna 1687..1695  
FT /tag= q  
FT /label= glycosylation site  
XX WO9105862-A.  
XX 02-MAY-1991.  
XX 20-OCT-1989; 89FR-00013770.  
XX 20-OCT-1989; 89FR-00013770.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Mogensen K, Lutfalla G, Gresser I;  
XX WPI; 1991-148740/20.  
XX P-PSDB; AAR11958.



XX New human alpha-interferon receptor protein - useful for testing  
PT interferon agonists and in treatment or diagnosis.  
XX

PS Disclosure; Fig 4; 30pp; French.

XX This sequence encodes a recombinant human alpha interferon (IFN) receptor  
CC protein useful for the testing of IFN agonists and for treatment and  
CC diagnosis of viral diseases and tumours. Antibodies raised against this  
CC protein can be used for blocking the receptor when required, e.g. where  
CC overexpression of alpha-IFN is harmful. The Abs are also useful for e.g.  
CC drug targeting. Variants of the protein, having residue 184 (Ihr)  
CC replaced by Arg and an Asp in- serted between residues 479 and 480, are  
XX also useful

SQ Sequence 2784 BP; 896 A; 553 C; 578 G; 757 T; 0 U; 0 Other;

Query Match 99.1%; Score 1330.8; DB 2; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCAGGAGTCTGGCGGCTCCAGATGATGGTCCTCCTGGGCGCGACGCCCTAG 60  
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QY 53 CTGTGGGATCTGGCGGCTCCAGATGATGGTCCTCCTGGGCGCGACGCCCTAG 112  
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QY 61 TGCTCGTCGCGCTGGGCGCCATGGGTGTTGCCGAGCGCGAGGTGGGAAAAATCTAAAT 120  
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QY 113 TGCTCGTCGCGCTGGGCGCCATGGGTGTTGCCGAGCGCGAGGTGGGAAAAATCTAAAT 172  
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DB |||||  
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DB |||||  
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DB |||||  
QY 601 TCTCACCAGAGACTACTTTATTTGCTTAAAGTTAAAGCAGCACTACTTACGTCTAGAAAA 660  
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DB |||||  
QY 713 TTGGTGTCTATAGTCCAGTACATTTGTATAAGACCAAGTGGAAAAATGAACCTACCTCCAC 772  
DB |||||  
QY 721 CAGAAATATAGAGTCCAGTCTCAAAATCAGACATATGTTCTTAAATGGGATATACAT 780  
DB |||||  
QY 773 CAGAAATATAGAGTCCAGTCTCAAAATCAGACATATGTTCTTAAATGGGATATACAT 832  
DB |||||

QY 781 ATCAAAACATGACCTTTCAAGTTTCAGTGGCTCCACGCTCTTTTAAAGAAATCTCTCGAA 840  
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QY 841 ACCATTTGTATTAATGGAACAAATACCTGACTGTGAAAATGTCAAAACCTACCCAGTGTG 900  
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QY 893 ACCATTTGTATTAATGGAACAAATACCTGACTGTGAAAATGTCAAAACCTACCCAGTGTG 952  
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QY 961 GAAATAACACATCTTTTGGTCTGGAAGAGATAAAGTTTGATCTGAAAATCAAGCTTTCC 1020  
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QY 1373 GAAATACCTCTAAA 1386  
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RESULT 15  
AAF16297  
ID AAF16297 standard; cDNA; 2017 BP.  
XX AC AAF16297;  
XX AC AAF16297;  
XX DT 13-MAR-2001 (first entry)  
XX DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:732.  
XX DE Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
XX KW neuroprotective; cytosolic; cardiocactive; immunomodulatory; muscular;  
XX KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
XX KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
XX KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
XX KW wound; infectious disease; ss.  
XX OS Homo sapiens.  
XX PN WO200055174-A1.  
XX PD 21-SEP-2000.  
XX PF 08-MAR-2000; 2000WO-US005988.  
XX PR 12-MAR-1999; 99US-0124270P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI (ROSE/) ROSEN C A.  
XX PI Rosen CA, Ruben SM;  
XX





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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 19:30:55 ; Search time 5826 Seconds  
(without alignments)  
10785.282 Million cell updates/sec

Title: US-10-824-981-1  
Perfect score: 1343  
Sequence: 1 ctccagggaatctgcggcgc.....ataccttaaatgaggtacc 1343

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_hc.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_est7.\*  
9: gb\_gss1.\*  
10: gb\_gss2.\*  
11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943.6	70.3	1042	5	BX417950 BX417950
2	840.8	62.6	1073	3	BM476333 AGENCOURT
3	800.8	59.6	1440	11	DQ035425 Homo sapi
4	756.2	56.3	876	5	BQ440937 AGENCOURT
5	750.8	55.9	807	1	AU133717 AU133717
6	721.8	53.7	820	2	BG613775 602639759
7	716.8	53.4	918	3	BM457086 AGENCOURT
8	713.2	53.1	1042	2	BE739817 601556144
9	692	51.5	880	1	AU136208 AU136208
10	680.2	50.6	930	3	BM465808 AGENCOURT
11	673.6	50.2	784	2	BG618347 602645709
12	662.4	49.3	843	6	CD109826 AGENCOURT
13	649.4	48.4	674	5	BX356887 DKFZp781N
14	633	47.1	699	1	AL707406 AL707406
15	632	47.1	678	6	CD697468 EST13991
16	631	47.0	920	3	BM452951 AGENCOURT
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18	629	46.8	651	7	CN425394 170005315
19	618.8	46.1	643	7	CV029361 8111 Full
20	618.6	46.1	868	2	BG506738 601861342
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22	602.6	44.9	810	3	BI463822 603202543

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27	557.4	41.5	570	3	BP207712
28	556.4	41.4	645	2	BE467210
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43	524	39.0	627	1	AU137565
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## ALIGNMENTS

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DEFINITION BX417950 Homo sapiens PLACENTA Homo sapiens CDNA clone CS0DE014YB03  
5-PRIME, mRNA sequence.  
ACCESSION BX417950  
VERSION BX417950.2 GI:46955956  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1042)  
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 15, 2003 this sequence version replaced gi:30767795.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
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into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library, a  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 10373.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DE014CA02QPI&c=10373.f.  
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

ORIGIN

Query Match		70.3%; Score 943.6; DB 5; Length 1042;
Best Local Similarity		97.4%; Pred. No. 5.9e-226;
Matches		968; Conservative 10; Mismatches 14; Indels 2; Gaps 2;
QY	1	CTCAGGGATCTCGGGGGCTCCAGATGATGTCCTCTCTGGGGCGACACCTTAG 60
DB	47	CTGGTGGGATCTCGGGGGCTCCAGATGATGTCCTCTCTGGGGCGACACCTTAG 106
QY	61	TGCTCTGTCGCGCGTGGCCATGGTGTGTCGCGAGCGCGAGTGGAAAAATCTAAAT 120
DB	107	TGCTCTGTCGCGCGTGGCCATGGTGTGTCGCGAGCGCGAGTGGAAAAATCTAAAT 166
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DB	167	CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCTGAGTGGAAACAGGA 226
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DB	227	GCATGAGTCTGCGGAATGTCATCTTTTCATTCGATATCAAAAAAATCTGGGATGGATA 286
QY	241	ATTGGATAAAATGTCCTGGGTGCAGAAATTAATCTAGTACCAATGCACTTTTCTTCAC 300
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QY	301	TCAAGCTGAATGTTATGAAGAAATTAATTTGGGTATAGAGCAGAAAAAGAAACACTT 360
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DB	407	CTTCATGTTAGAGTTGATCTCATTTTACACATTTGCAAAAGTTCAGATGGTCTCTCCAG 466
QY	421	AAGTACATTTAGAGCTGAAGTAAGCAATAGTGTATACATCTCTCTGGAAACAAAG 480
DB	467	AAGTACATTTAGAGCTGAAGTAAGCAATAGTGTATACATCTCTCTGGAAACAAAG 526
QY	481	ATAGTGTATGTCGGCTTTTGGATGTTTAACTTTATCATATAGTCTTATCTGGAATA 540
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QY	541	ACTCTTCAGGTGAGAAAGGATGAAATATTTATTCAGACATATAAATTTATAAAC 600
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DB	647	TCTCACGAGACTACTTATTTCTAAAGTTAAAGCAGCACTTACGTCTATGGAAA 706
QY	661	TTGGTGTCTATAGTCCAGTACATTTGTATAAGACCACAGTTGAAAATGAACTACCTCCAC 720
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QY	721	CAGAAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780
DB	767	CAGAAAATATAGAAGTCAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 826
QY	781	ATCGAACAATGACCTTTCAGTTCAGTGTCTCCAGCCTTTTAAAGGAATCTCTGGAA 840
DB	827	ATCGAACAATGACCTTTCAGTTCAGTGTCTCCAGCCTTTTAAAGGAATCTCTGGAA 886
QY	841	ACCATTTGTATAAATGAAAACAAATACCTGACTGT - GAAAATGTCAAAATCTACCAAGTGT 899
DB	887	ACCATTTGTATAAATGAAAACAAATACCTGACTGTGTGGAANAATGTCAAACTACCAAGTGT 946
QY	900	GTCTTTCTCAAAACGTTTTCAAAAGAAATTTACCTTCTCGCGGTACAAAGCATCTGAT 959
DB	947	GTCTTTCTCAAAACGTTTTCAAAAGAG - AWTATCCTTCYCCGCGTACAAACATCTGAT 1005
QY	960	GGAAATAACACATCTTTTGGTCTGAGAGATAA 993
DB	1006	GGAAATAACACATCTTTTGGTCTGAGAGATAA 1039

RESULT 2  
BM476333  
LOCUS  
DEFINITION  
5', mRNA sequence.  
AGENCOURT\_6479121 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:558971  
BM476333  
VERSION  
BM476333.1 GI:18525375  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1073)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
UNPUBLISHED (1999)  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Cloned by: Agencourt Bioscience Corporation  
Cloned distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL2282 row: m column: 20  
High quality sequence stop: 736.  
Location/Qualifiers  
1..1073  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:558971"  
/tissue\_type="duodenal adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 88"  
/note="Organ: small intestine; Vector: pCMV-SPORT6;  
Site\_1: Noti; Site\_2: SalI; Cloned unidirectionally;  
oligo-dr primed. Average insert size 1.767 kb. Library  
enriched for full-length clones and constructed by Life  
Technologies. Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 62.6%; Score 840.8; DB 3; Length 1073;  
Best Local Similarity 94.1%; Pred. No. 4.1e-200;  
Matches 928; Conservative 0; Mismatches 49; Indels 9; Gaps 5;  
QY 1 CTGACGGGATCTCGCGGGCTCCAGATGATGTCCTCTCTGGGGCGACACCTTAG 60  
DB 66 CTGGTGGGATCTGCGGGCTCCAGATGATGTCCTCTCTGGGGCGACACCTTAG 125  
QY 61 TGCTCTGTCGCGTGGGCCCATGGGTGTCGCGAGCGCGAGTGGAAAAATCTAAAT 120  
DB 126 TGCTCTGTCGCGTGGGCCCATGGGTGTCGCGAGCGCGAGTGGAAAAATCTAAAT 185  
QY 121 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCTGAGTGGAAACAGGA 180  
DB 186 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTCTGAGTGGAAACAGGA 245  
QY 181 GCATGAGTCTGTCGGGAATGTGACCTTTTTCATTCGATTTCAAAAACTGGGATGGATA 240  
DB 246 GCGATGAGTCTGTCGGGAATGTGACCTTTTTCATTCGATTTCAAAAACTGGGATGGATA 305  
QY 241 ATTGGATAAAATGTCCTGGGTGCAGAAATTAATCTAGTACCAATGCACTTTTCTTCAC 300  
DB 306 ATTGGATAAAATGTCCTGGGTGCAGAAATTAATCTAGTACCAATGCACTTTTCTTCAC 365  
QY 301 TCAGCTGATGTTTATGAAGAAATTAATTTGGGTATAGAGCAGAAAAAGAAACACTT 360  
DB 366 TCAGCTGATGTTTATGAAGAAATTAATTTGGGTATAGAGCAGAAAAAGAAACACTT 425  
QY 361 CTTTCATGATGAGGTTGACTCATTTTACACCAATTTTCGCAAGCTCAGATTTGGTCTCCAG 420



QY	867	CCTGACGTGTGAAATGTCAAACTACCCAGTGTCTTTCTCCTCAAAACGTTTTCCAAAA	926
Db	841	CCTGACTGTGAAATGTCAAACTACCCAGTGTCTTTCTCCTCAAAACGTTTTCCAAAA	900
QY	927	GGAAATTTACCTTCTCCGCGTACAGCATCTGATGGAATAACACATCTTTTGGTCTGAA	986
Db	901	GGAAATTTACCTTCTCCGCGTACAGCATCTGATGGAATAACACATCTTTTGGTCTGAA	960
QY	987	GAGATAAAGTTTGATCTACTGAAATACAAAGCTTTCTACTCTCCTCAGTCTTTTAAACATTAGA	1046
Db	961	GAGATAAAGTTTGATCTACTGAAATACAAAGCTTTCTACTCTCCTCAGTCTTTTAAACATTAGA	1020
QY	1047	TCCTTTAGTCATTCATTCCTATCTATATATCGGTGCTCCAAAAACAGTCTGGAACACGCCT	1106
Db	1021	TCCTTTAGTCATTCATTCCTATCTATATATCGGTGCTCCAAAAACAGTCTGGAACACGCCT	1080
QY	1107	GTGATCCAGCATTCACCATGATTATGAAATTTATTTTGGGAAACACATTCAAATGCT	1166
Db	1081	GTGATCCAGCATTCACCATGATTATGAAATTTATTTTGGGAAACACATTCAAATGCT	1140
QY	1167	GAGAGAAAAATTTATCGAGAAAAAACTGATGTTTACAGTTCCTTAATTTGAAACCACTGACT	1226
Db	1141	NN	1200
QY	1227	GTATATTGTGTGAAAGCAGACACACACCATCGATGAAAGCTGAATAAAGCAGTGT	1286
Db	1201	NN	1260
QY	1287	TTTAGTGACCTGTATGTGAGAAAAACAAACAGGAAATACCTCTTAA	1334
Db	1261	NN	1308
RESULT 4			
BO440937			
LOCUS	BO440937	876 bp	mRNA
DEFINITION	AGENCOURT_7914300 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6156931	linear	EST 24-MAY-2002
ACCESSION	BO440937		
VERSION	BO440937.1	GI:21180013	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 876)		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13501 row: p column: 20 High quality sequence stop: 628.		
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source	1..876		
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	/clone="IMAGE:6156931"		
	/tissue_type="leiomyosarcoma"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH_MGC_71"		
	/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2.1 kb."		

ORIGIN			
Query Match	56.3%;	Score 756.2;	DB 5; Length 876;
Best Local Similarity	98.7%;	Pred. No. 7.4e-179;	
Matches 761;	Conservative 0;	Mismatches 10;	Indels 0; Gaps 0;
QY	1	CTGACGGGATCTGCGCGGCTCCACAGATGATGTCCTCTCTGGGCGGACGACCCCTAG	60
Db	70	CTGGTGGGATCTGCGCGGCTCCACAGATGATGTCCTCTCTGGGCGGACGACCCCTAG	129
QY	61	TGCTCTGTCGCGTGGGCCCATGGGTGTTGTCGCGACCGGAGGTGGAATAAATCTAAAT	120
Db	130	TGCTCTGTCGCGTGGGCCCATGGGTGTTGTCGCGACCGGAGGTGGAATAAATCTAAAT	189
QY	121	CTCCTCAAAAAGTACAGAGTTCGACATCATAGATGACAACTTTATCTCTGAGGTGGAACAGGA	180
Db	190	CTCCTCAAAAAGTACAGAGTTCGACATCATAGATGACAACTTTATCTCTGAGGTGGAACAGGA	249
QY	181	GGATGAGTCTGTGCGGAAATGTGACCTTTTTCATTCGATTATCAAAAAAATCTGGGATGGATA	240
Db	250	GGATGAGTCTGTGCGGAAATGTGACCTTTTTCATTCGATTATCAAAAAAATCTGGGATGGATA	309
QY	241	ATTGGATAAAATGTCCTGGGTGTCAGAAATATTACTAGTACCAAAATGCAACTTTTCTTAC	300
Db	310	ATTGGATAAAATGTCCTGGGTGTCAGAAATATTACTAGTACCAAAATGCAACTTTTCTTAC	369
QY	301	TCAGCTGTAATGTTTATGAAGAAATTTAAATTCGTTATAGAGCAGAGAAAGAAACACTT	360
Db	370	TCAGCTGTAATGTTTATGAAGAAATTTAAATTCGTTATAGAGCAGAGAAAGAAACACTT	429
QY	361	CTTCATGTTATGAGGTTGACTCATTTACACCAATTTCCGCAAGCTCAGATTGGTCTCCAG	420
Db	430	CTTCATGTTATGAGGTTGACTCATTTACACCAATTTCCGCAAGCTCAGATTGGTCTCCAG	489
QY	421	AGTACATTTAGAGCTGAAGTAAGCAATAGTGATACACATCTCTCTCTGGAAACAAAAG	480
Db	490	AGTACATTTAGAGCTGAAGTAAGCAATAGTGATACACATCTCTCTCTGGAAACAAAAG	549
QY	481	ATAGTGTATGCGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAATA	540
Db	550	ATAGTGTATGCGGCTTTGGATGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAATA	609
QY	541	ACTCTTCAGGTGTAGAAGAAAGGATTGAAAAATATTTATCCAGACATAAAATTTATAAAC	600
Db	610	ACTCTTCAGGTGTAGAAGAAAGGATTGAAAAATATTTATCCAGACATAAAATTTATAAAC	669
QY	601	TCTCACCAGAGACTACTTATTTGCTTAAAGTTTAAAGCAGCACTACTTACGTCTATGGAATA	660
Db	670	TCTCACCAGAGACTACTTATTTGCTTAAAGTTTAAAGCAGCACTACTTACGTCTATGGAATA	729
QY	661	TTGGTGTCTATAGTCCAGTACATTTGTTATTAAGACCAAGTTTGAATAATGAACCTACCTCCAC	720
Db	730	TTGGTGTCTATAGTCCAGTACATTTGTTATTAAGACCAAGTTTGAATAATGAACCTACCTCCAC	789
QY	721	CAGAAATATAGAAGTCAGTGTCCAAATATTTTATCCAGACATAAAATTTATAAAC	771
Db	790	CAGAAATATAGAAGTCAGTGTCCAAATATTTTATCCAGACATAAAATTTATAAAC	840
RESULT 5			
AUI33717			
LOCUS	AUI33717	807 bp	mRNA
DEFINITION	AUI33717	OVARC1 Homo sapiens cDNA clone	linear
ACCESSION	AUI33717		EST 01-AUG-2002
VERSION	AUI33717.1	GI:10994256	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 807)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.  
 TITLE HRI human cDNA project  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp  
 HRI human cDNA project; 5'- and 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES  
 source  
 1. .807  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="OVARC1000513"  
 /tissue type="ovary, tumor tissue"  
 /clone\_lib="OVARC1"  
 /note="Vector: pME18SFL3"

ORIGIN  
 Query Match 55.9%; Score 750.8; DB 1; Length 807;  
 Best Local Similarity 99.4%; Pred. No. 1.7e-177;  
 Matches 774; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

558 GAAAGGATTGAAATATTATTTC-AGACATAAAATTTATAAATCTCCACGAGACTAC 616  
 Db  
 1 GAAAGGATTGAAATATTATTTC-CAAGACATATAAAATTTATAAATCTCCACGAGACTAC 60  
 Qy  
 617 TTATGTCTAAAGCTTAAAGCAGCAGCTACTTACGTCATGGAATTCGGTCTATAGTCC 676  
 Db  
 61 TTATGTCTAAAGCTTAAAGCAGCAGCTACTTACGTCATGGAATTCGGTCTATAGTCC 120  
 Qy  
 677 AGTACATTGTATAAGACCAGTGTGAAATGAACTACCTCCACGAGAAATATAGAGT 736  
 Db  
 121 AGTACATTGTATAAGACCAGTGTGAAATGAACTACCTCCACGAGAAATATAGAGT 180  
 Qy  
 737 CAGTGTCAAATCAGAACTATGTTCTTAAATGGGATTATACATGATGAAACATGACGTT 796  
 Db  
 181 CAGTGTCAAATCAGAACTATGTTCTTAAATGGGATTATACATGATGAAACATGACGTT 240  
 Qy  
 797 TCAAGTTTCAGTGGCTCCACGCTTTTAAAGGAATCCCTGGAACCACTTTGTATAATG 856  
 Db  
 241 TCAAGTTTCAGTGGCTCCACGCTTTTAAAGGAATCCCTGGAACCACTTTGTATAATG 300  
 Qy  
 857 GAAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTGTTCTTCTCAAACGT 916  
 Db  
 301 GAAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTGTTCTTCTCAAACGT 360  
 Qy  
 917 TTTCAAAAGGAATTTACCTTCCGCGTCAAGCATCTGATGAAATACACATCTTT 976  
 Db  
 361 TTTCAAAAGGAATTTACCTTCCGCGTCAAGCATCTGATGAAATACACATCTTT 420  
 Qy  
 977 TTGCTCTGAGAGATAAGTTTGATCTGAAATACAGCTTCTCTCTCCAGTCTT 1036  
 Db  
 421 TTGCTCTGAGAGATAAGTTTGATCTGAAATACAGCTTCTCTCTCCAGTCTT 480  
 Qy  
 1037 TAACATTAGATCCCTTAGTGATTCAATTCATATCTATATCGGTGTCCTCAAACAGTCTGG 1096  
 Db  
 481 TAACATTAGATCCCTTAGTGATTCAATTCATATCTATATCGGTGTCCTCAAACAGTCTGG 540  
 Qy  
 1097 AAACACGCTGTGATCCAGGATTAFCACCTGATTTATGAAATATTTTTCGGAAAAAC 1156  
 Db  
 541 AAACACGCTGTGATCCAGGATTAFCACCTGATTTATGAAATATTTTTCGGAAAAAC 600  
 Qy  
 1157 TTCAATGCTGAGAGAAAAATTTTCGAGAAAAAACTGATGTTACGTTCTTAATTGAA 1216

Db 601 TTCAATGCTGAGAGAAAAATTTTCGAGAAAAAACTGATGTTACGTTCTTAATTGAA 660  
 Qy 1217 ACCACTGACTGTATATTGTGAAAGCCAGCAGCACACCATGATGAAAGCTGAATAA 1276  
 Db 661 ACCACTGACTGTATATTGTGAAAGCCAGCAGCACACCATGATGAAAGCTGAATAA 720  
 Qy 1277 AAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACC-AGGAAATACCTCTAAA 1334  
 Db 721 AAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACCAGGAATACCTCCAA 779

RESULT 6  
 BG613775  
 LOCUS 820 bp mRNA linear EST 18-APR-2001  
 DEFINITION 602639759F1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4770807 5', mRNA sequence.  
 ACCESSION BG613775  
 VERSION BG613775.1 GI:13665146  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 820)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 Email: rgs@bbs-rmail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1638 row: e column: 16  
 High quality sequence stop: 775.

FEATURES  
 source  
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 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue type="embryonal carcinoma"  
 /lab host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_61"  
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggccgctcgcc); Site\_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 53.7%; Score 721.8; DB 2; Length 820;  
 Best Local Similarity 96.5%; Pred. No. 3.2e-170;  
 Matches 780; Conservative 0; Mismatches 23; Indels 5; Gaps 4;

Qy 59 AGTGCTCGTCGCCGTCGGCCCATGGTGTTCGCGAGCCGCGAGTGGAAAAATCTAAA 118  
 Db 2 AGTGCTCGTCGCCGTCGGCCCATGGTGTTCGCGAGCCGCGAGTGGAAAAATCTAAA 60  
 Qy 119 ATCTCTCTCAAAAAGTAGAGGTGCGATCATAGATGACAACTTTATCTGAGGTGGAAACAG 178  
 Db 61 ATCTCTCAAAAAGTAGAGGTGCGATCATAGATGACAACTTTATCTGAGGTGGAAACAG 120

179 GAGCGATGAGTCTGTGCGGAATGAGACTTTTTCATTCGATATATCAAAAACTGGATGGA 238  
121 GAGCGATGAGTCTGTGCGGAATGAGACTTTTTCATTCGATATATCAAAAACTGGATGGA 180  
239 TAATTGGATAAAATGCTGGGTGTCAGATATATCTAGTACCAATGCAACTTTTCTTC 238  
181 TAATTGGATAAAATGCTGGGTGTCAGATATATCTAGTACCAATGCAACTTTTCTTC 240  
299 ACTCAAGCTCAATGTTTATGAAGAAATTAATTCGATATAGAGCAGAAAAAGAAACAC 358  
241 ACTCAAGCTCAATGTTTATGAAGAAATTAATTCGATATAGAGCAGAAAAAGAAACAC 300  
359 TTCTTCATGATGAGTTCAGCTCATTTACACCAATTCGCAAAAGCTCAGATTCGTCCTCC 418  
301 TTCTTCATGATGAGTTCAGCTCATTTACACCAATTCGCAAAAGCTCAGATTCGTCCTCC 360  
419 AGAAGTACATTTAGAGCTGAAGTAAGCAATAGTGATACACATCTCTCTGGAACAAA 478  
361 AGAAGTACATTTAGAGCTGAAGTAAGCAATAGTGATACACATCTCTCTGGAACAAA 420  
479 AGATAGTGTATGTTGGCTTTGATGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAA 538  
421 AGATAGTGTATGTTGGCTTTGATGTTTAAAGCTTTTACATATAGCTTACTTATCTGGAA 480  
539 AAACTCTTCAGGTGTAGAGAAAGGATTTGAAATATTTTATTCAGACATATAAATTTATAA 598  
481 AAACTCTTCAGGTGTAGAGAAAGGATCGAAATATTTTATTCAGACATATAAATTTATAA 540  
599 ACTCTACACGAGACTACTTATGTTCTAAAAGTTAAAGAGCAGCTACTTACGTCATGGAA 658  
541 AGTCTACACGAGACTACTTATGTTCTAAAAGTTAAAGAGCAGCTACTTACGTCATGGAA 600  
659 AATTGGTGTCTATAGTCCAGTACATGTTATAAGACCAACAGTTCGAAATCAACTACTCTCC 718  
601 AATCGGTGTCTATAGTCCAGTACATGTTATAAGACCAACAGTTCGAAATCAACTACTCTCC 660  
719 ACCAGAAATATAGAGTCTAGTGTCCAAATATC-AGAACTATGTTCTT--AAATGGGATTA 775  
661 GACAGAAATATAGAGTCTAGTGTCCAAATATCAGAACTATGTTCTTACATGGGATTA 720  
776 TACATATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCTTTTAAAAAGGAATCC 835  
721 TACATATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGCTTTTAAAAAGGAAT-C 779  
836 TGGAAACCATTTGTATATAATGGAACAA 863  
780 TGGGAACCATTTGTATAATGGAACAA 807

RESULT 7  
BM457086  
LOCUS  
DEFINITION  
5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BM457086 918 bp mRNA linear EST 05-FEB-2002  
AGENCOURT\_6411670 NIH\_MGC\_92 Homo sapiens cdna clone IMAGE:5583330  
BM457086  
BM457086.1 GI:18506126  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 918)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)  
Tissue Procurement: ATCC  
cdna Library Preparation: Life Technologies, Inc.  
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: LLAM12346 row: d column: 19  
High quality sequence stop: 636.  
Location/Qualifiers  
1..918  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5583330"  
/tissue\_type="embryonal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_92"  
/note="Organ: Testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 53.4%; Score 716.8; DB 3; Length 918;  
Best Local Similarity 98.9%; Pred. No. 6e-169; 7; Indels 1; Gaps 1;  
Matches 732; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
QY 586 ATAAAAATTTATAAACTCTCACGAGACTACTTATTGTCTAAAAAGTTAAAGCAGCACTAC 645  
DB 1 ATAAAAATTTATAAACTCTCACGAGACTACTTATTGTCTAAAAAGTTAAAGCAGCACTAC 60  
QY 646 TTACGTCATGGAAAAATTTGGTGTCTATAGTCCAGTACATTTGATAAAGACCAACAG- TTGAA 704  
DB 61 TTACGTCATGGAAAAATTTGGTGTCTATAGTCCAGTACATTTGATAAAGACCAACAGTAA 120  
QY 705 AATGAACTACCTCCACGAGAAATATAGAGTCAGTGTCCAAATCAGAACTATGTTCTT 764  
DB 121 AATGAACTACCTCCACGAGAAATATAGAGTCAGTGTCCAAATCAGAACTATGTTCTT 180  
QY 765 AAATGGGATTTATACATATGCAACATGACCTTTTCAAGTTTCAGTGGCTCCACGCTTTT 824  
DB 181 AAATGGGATTTATACATATGCAACATGACCTTTTCAAGTTTCAGTGGCTCCACGCTTT 240  
QY 825 AAAAGGAATCTCGAAACCAATTTGTATAAATGGAAACAAATACCTGCTGTAATAATGTC 884  
DB 241 AAAAGGAATCTCGAAACCAATTTGTATAAATGGAAACAAATACCTGCTGTAATAATGTC 300  
QY 885 AAAAATACCCAGTGTCTTCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGC 944  
DB 301 AAAAATACCCAGTGTCTTCTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCCGC 360  
QY 945 GTACAAGCATCTGATGGAATAACACATCTTTTGTCTGAGAGAGATAAAGTTTGATACT 1004  
DB 361 GTACAAGCATCTGATGGAATAACACATCTTTTGTCTGAGAGAGATAAAGTTTGATACT 420  
QY 1005 GAAATACAGCTTTCTCTACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGAATCATT 1064  
DB 421 GAAATACAGCTTTCTCTACTTCTCCAGGCTTTTAAACATTAGATCCCTTAGTGAATCATT 480  
QY 1065 CATATCTATATCGGTGCTCCAAAACAGTCTGGAAACAGCTGTGATCCAGGATATCCA 1124  
DB 481 CATATCTATATCGGTGCTCCAAAACAGTCTGGAAACAGCTGTGATCCAGGATATCCA 540  
QY 1125 CTGATTTATGAATAATTTTGGGAAAAACACTTCAAAATGCTCAGAGAAAAATTTATCGAG 1184  
DB 541 CTGATTTATGAATAATTTTGGGAAAAACACTTCAAAATGCTCAGAGAAAAATTTATCGAG 600  
QY 1185 AAAAAAATGATGTTTACAGTTCCTAAATTTGAAACCACTGATATATTTGTTGTAAGGCC 1244  
DB 601 AAAAAAATGATGTTTACAGTTCCTAAATTTGAAACCACTGATATATTTGTTGTAAGGCC 660  
QY 1245 AGAGCACACCACTGATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGCCTGTATGT 1304  
DB 661 AGAGCACACCACTGATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGCCTGTATGT 720



Qy	1305	GAGAAACAAAACCAGGAAA	1324
Db	721	GAGAAACAAAACCAGGAAA	740
RESULT 8			
BE739817/c			
LOCUS	BE739817	1042 bp mRNA linear	EST 15-SEP-2000
DEFINITION	601556144T1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825850 3', mRNA sequence.		
ACCESSION	BE739817		
VERSION	BE739817.1	GI:10153809	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1042)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-f@mail.nih.gov Tissue Procurement: ARCC cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLC492 row: h column: 11 High quality sequence start: 30 High quality sequence stop: 710.		
FEATURES			
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	/clone="IMAGE:3825850"		
	/tissue_type="hypernephroma"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/clone_lib="NIH MGC 58"		
	/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgcttcgccc); Site 2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dT(30)BN-3' (where B = A, C, G or N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."		
ORIGIN			
Query Match	53.1%;	Score 713.2;	DB 2; Length 1042;
Best Local Similarity	94.5%;	Pred. No. 4.9e-168;	
Matches	805; Conservative	0; Mismatches 38; Indels	9; Gaps 6;
Qy	422	AGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATAC-ACATCTCTCTCGAACAAG	480
Db	851	AGCACTTTACGCACTTAATAAGGCAATAGTGACACAACTTCTCTCTCGAACAAG	792
Qy	481	ATAGTGTATGTGGCTTTGGATGGTTTAA-GCTTTACATATAGCTTACTTA---TCTGG	536
Db	791	ATAGTGTATGTGGCTTTGGATGGTTTAAAGGCTTTTACATATAGCTTAATCTGGGA	732
Qy	537	AAAAAATCTTCAGCTGTAG-AAGAAAGGATTGAAATATTTATTCAGACATATAATTTA	595
Db	731	AAAAAATCTTCAGCTGTAGAAAGGATTGAAATATTTATTCAGACATATAATTTA	672
Qy	596	TAAACTCTCACCAGAGACTACTTTATGTCTTAAAGTTAAAGCAGCAGCACTACTTACGTCATG	655

Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
Location/Qualifiers  
1. .880  
/organism="Homo sapiens"  
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/clone="PLA1003742"  
/tissue\_type="placenta"  
/clone\_lib="PLA1"  
/note="Vector: pME18SFL3"

FEATURES  
source  
ORIGIN  
Query Match 51.5%; Score 692; DB 1; Length 880;  
Best Local Similarity 94.0%; Pred. No. 1e-162;  
Matches 803; Conservative 0; Mismatches 38; Indels 13; Gaps 8;  
QY 1 CTGCAGGATCTCGCGCGCTCCAGATGATGGTCCTCTGGGCGGCGACGACCTAG 60  
DB 15 CTGGTGGATCTCGCGCGCTCCAGATGATGGTCCTCTGGGCGGCGACGACCTAG 74  
QY 61 TGCTCGTCGCGCGTGGGCCCATGGTGTTCGCGAGCGGCGAGGTGGAAAAATCTAAAT 120  
DB 75 TGCTCGTCGCGTGGGCCCATGGTGTTCGCGAGCGGCGAGGTGGAAAAATCTAAAT 134  
QY 121 CTCTCAAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGTGAACAGGA 180  
DB 135 CTCTCAAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGCGGAACAGGA 194  
QY 181 GCGATGAGTCTGTCGGGAATGTCATTTTCATTCGATATCAAAAATCTGGATGATA 240  
DB 195 GCGATGAGTCTGTCGGGAATGTCATTTTCATTCGATATCAAAAATCTGGATGATA 254  
QY 241 ATTGGATAAAATGTCTGGGTGTCAGAAATTAAGTACCAATGCACTTTCTTCAC 300  
DB 255 ATTGGATAAAATGTCTGGGTGTCAGAAATTAAGTACCAATGCACTTTCTTCAC 314  
QY 301 TCAAGCTGAATGTTATGAAGAAATTAATTTGGTATGAAGCAGAAAAAGAAACACTT 360  
DB 315 TCAAGCTGAATGTTATGAAGAAATTAATTTGGTATGAAGCAGAAAAAGAAACACTT 374  
QY 361 CTTTCATGATGAGTGTGACTCTTACACATTTGCAAGCTCAGATTGGTCTCCAG 420  
DB 375 CTTTCATGATGAGTGTGACTCTTACACATTTGCAAGCTCAGATTGGTCTCCAG 434  
QY 421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTATACATCTCTCTGGAAACAAAG 480  
DB 435 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTATACATCTCTCTGGAAACAAAG 494  
QY 481 ATAGTGTATGTGGCTTTGGATGGTTTAACTTTACATATAGCTTACTTCTGAAAAA 540  
DB 495 ATAGTGTATGTGGCTTTGGATGGTTTAACTTTACATATAGCTTACTTCTGAAAAA 554  
QY 541 ACTCTTCAGGTGTAGAAAGAGATTCAGAAATATTTATTCAGACATATAAATTTATAAC 600  
DB 555 ACTCTTCAGGTGTAGAAAGAGATTCAGAAATATTTATTCAGACATATAAATTTATAAC 614  
QY 601 TCTCACCAGAGCTACTTATTTGTCTAAAGTTAAAGC-AGCAGCTTACTAGTCAAT-GGAA 658  
DB 615 TCTCACCAGAGCTACTTATTTGTCTAAAGTTAAAGCAGCACTACTTACTCATGGAA 674  
QY 659 AATTGGTGTCTATAGTCCAGTACATTTGTAT-AAAGCCAG-TTGAAATGAACTACCT 716  
DB 675 AATTGGTGTCTAAAGTCCAAATATTTATTAAGAGCCACAGTTTGAATAAGAACTACCT 734  
QY 717 CCACCA--GAAAAATATAGAGTCAAGTCCAAATATTAAGAGCTA--TGTCTTAAATGGGA 772  
DB 735 CCACCAAGAAATATTAAGTCAAGTCCAAATATTAAGAGCTAATGTTCTTAAATNGG 794  
QY 773 TTATACATATGC--AAACATGACCTTTCAAGTTCAAGTGG--CTCCACGCTTTTAAAAA 827

Db 795 ATATNCATATTCAAACATTTCAAGTTCAGTGGCTCCAGNCTTTTAAAAA 854  
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Db 855 AGGAATCCTNGAA 868

RESULT 10  
BM465808  
LOCUS  
DEFINITION  
AGENCOURT\_6423633 NIH\_MGC\_67 Homo sapiens cDNA clone IMAGE:5580652  
5', mRNA sequence.  
BM465808  
BM465808.1 GI:18514850  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 938)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM121339 row: e column: 05  
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Location/Qualifiers  
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/clone\_lib="NIH MGC 67"  
/notes="Organ: eye; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Library constructed by Life  
Technologies."

ORIGIN  
Query Match 50.6%; Score 680.2; DB 3; Length 938;  
Best Local Similarity 96.4%; Pred. No. 9.5e-160;  
Matches 706; Conservative 0; Mismatches 24; Indels 2; Gaps 1;  
QY 1 CTGACGAGATCTCGCGCGCTCCAGATGATGGTCCTCTGGGCGGCGACGACCTAG 60  
DB 55 CTGGTGGATCTCGCGCGCTCCAGATGATGGTCCTCTGGGCGGCGACGACCTAG 114  
QY 61 TGCTCTCGCGGTGGGCCCATGGGTGTTCGCGAGCGGCGAGGTGAAAAATCTAAAT 120  
DB 115 TGCTCTCGCGGTGGGCCCATGGGTGTTCGCGAGCGGCGAGGTGAAAAATCTAAAT 174  
QY 121 CTCTCAAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGTGAACAGGA 180  
DB 175 CTCTCAAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGTGAACAGGA 234  
QY 181 GCGATGAGTCTGTCGGGAATGTGACATTTTCATTCGATATCAAAAATCTGGATGATA 240  
DB 235 GCGATGAGTCTGTCGGGAATGTGACATTTTCATTCGATATCAAAAATCTGGATGATA 294  
QY 241 ATTGGATAAAATGTCTGGGTGTCAGAAATTAAGTACCAATGCACTTTCTTCAC 300

Db 295 ATTGATTAATTTGCTGGGTGTCAGATATATTACTAGTACCAATGCACTTTTCTTCCAC 354  
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATGAAGCGAGAAAGAAACACTT 360  
Db 355 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATGAAGCGAGAAAGAAACACTT 414  
Qy 361 CTTCAAGCTGATGAGGTTGACTCATTTACACCAATTTGCGAAAGCTCAGATTTGCTCTCCAG 420  
Db 415 CTTCAAGCTGATGAGGTTGACTCATTTACACCAATTTGCGAAAGCTCAGATTTGCTCTCCAG 474  
Qy 421 AAGTACATTTAGAAGCTGAAGATAAGCAATAGTGATACACATCTCTCTCGAAACAAAG 480  
Db 475 AAGTACATTTAGAAGCTGAAGATAAGCAATAGTGATACACATCTCTCTCGAAACAAAG 534  
Qy 481 ATAGTGTTATGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 540  
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Qy 661 TTGGTGCTATAGTCCAGTACATT--GTAATAAGACACAGTTGAAATGAATGAATACCTCC 718  
Db 715 TTGGTGCTATAGTCCAGTACATT--GTAATAAGACACAGTTGAAATGAATGAATACCTCC 774  
Qy 719 ACCAGAAATAT 730  
Db 775 CCCCAAAAAAT 786

RESULT 11  
LOCUS BG618347 784 bp mRNA linear EST 18-APR-2001  
DEFINITION 60264570991 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:4767243 5',  
mRNA sequence.

ACCESSION BG618347  
VERSION BG618347.1 GI:13669718  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 784)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CLONETECH Laboratories, Inc.  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.llnl.gov>

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/clone\_lib="NIH\_MGC\_76"  
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggcccgcctcgcc); Site\_2: SfiI (ggccattatggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGGCCATTTGCCC-3', and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGGCGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 50.2%; Score 673.6; DB 2; Length 784;  
Best Local Similarity 97.1%; Pred. No. 4.2e-158;  
Matches 707; Conservative 0; Mismatches 19; Indels 2; Gaps 2;  
Qy 1 CTG CAGGAGATCTGGCGGCTCCAGATGATGCTCTCTCTGGCGCGAGACCTTAG 60  
Db 51 CTGGTGGGATCTGGCGGCTCCAGATGATGCTCTCTCTGGCGCGAGACCTTAG 110  
Qy 61 TGCTCGTCGCGCTGGCGCCATGGGTGTTGTCGCGAGCGCAGGTGGAAAAATCTAAAT 120  
Db 111 TGCTCGTCGCGCTGGCGCCATGGGTGTTGTCGCGAGCGCAGGTGGAAAAATCTAAAT 170  
Qy 121 CTCTCTCAAAAAAGTAGAGTTCGACATCATAGATGACAACTTTATCTGAGGTGGAAACAGA 180  
Db 171 CTCTCTCAAAAAAGTAGAGTTCGACATCATAGATGACAACTTTATCTGAGGTGGAAACAGA 230  
Qy 181 GCGATGATCTCTGGGAAATGTGACTTTTTCATTCGATATCAAAAAACTGGATGGATA 240  
Db 231 GCGATGATCTCTGGGAAATGTGACTTTTTCATTCGATATCAAAAAACTGGATGGATA 290  
Qy 241 ATTGGATAAAATTCCTGGGTGTCAGAAATTTACTAGTACCATAATGCAACTTTTCTTCCAC 300  
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Qy 301 TCAAGCTGAATGTTTATGAAGAAATTTAAATTCGTTAAGAGCAGAAAAAGAAACACTT 360  
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Qy 361 CTTCAAGTATGAGGTGACTCATTTACACCAATTTGCGAAAGCTCAGATTTGCTCTCCAG 420  
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Db 471 AAGTACATTTAGAAGCTGAAGATAAGCAATAGTGATACACATCTCTCTCGAAACAAAG 530  
Qy 481 ATAGTGTTATGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 540  
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Qy 541 ACTCTTCAGGTGTAGAAGAAAGGATTGAAATATATTATTTCCAGACA-TAAATTTATAAA 599  
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Qy 600 CTCTCACCAGAGACTACTTATTTGCTTAAAGTTTAAAGCAGCAGCTACTTACGTCATGGAA 659  
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Qy 660 ATTGCTGTCTATAGTCCAGTACATTTGTTATAAAGACACAGTTGA-AAATGAATCACTCC 718  
Db 711 ATGGTGTTCTATAGTCCAGTACATTTGTTATAAAGACACAGTTGAACACTGACTACTCC 770  
Qy 719 ACCAGAA 726  
Db 771 ACCAGAA 778

RESULT 12  
LOCUS CD109826

DEFINITION AGNCOURT\_13889830 NIH\_MGC\_147 Homo sapiens cDNA clone  
IMAGE:3035602 5', mRNA sequence.  
ACCESSION CD109826

CD109826 843 bp mRNA linear EST 15-MAY-2003

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VERSION CD109826.1 GI:30754035
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 843)
          NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgaps-remail.nih.gov
          Tissue Procurement: Dr. Stefan Hansson
          and advice from Piero Carninci (RIKEN)
          cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: NDAM383 row: m column: 03
          High quality sequence stop: 489.
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                     /tissue_type="Human Placenta"
                     /lab_host="DH10B Tona"
                     /clone_lib="NIH_MGC_147"
                     /note="Organ: placenta; Vector: pBluescriptR; Site_1:
                     all-XhoI; Site_2: BamHI; Oligo-dr primed using primer
                     5'-TTTTTTTTTTTTTNN-3', size-selected for average
                     insert size 2.3 kb and normalized to ROT 5. This is a
                     primary library enriched for full-length clones and
                     constructed using the Cap-trapper method (Carninci, in
                     preparation). Library constructed by M. Brownstein, in
                     (NIH)/NHGRI, National Institutes of Health". Note: This is
                     a NIH_MGC library."
ORIGIN
Query Match          49.3%; Score 662.4; DB 6; Length 843;
Best Local Similarity 98.0%; Pred. No. 2.8e-155;
Matches 691; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 25 AGATGATGGTCTCTCTCTGGCGCGACGACCCCTAGTGTCTGTCGCGCGGCCCATGGG 84
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Db 29 AGATGATGGTCTCTCTCTGGCGCGACGACCCCTAGTGTCTGTCGCGCGGCCCATGGG 88
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QY 85 TGTGTCTGGCGCGCGAGGTGGAAAAATCTAAATCTCTCAAAAAGTAGAGTCGACA 144
    |||
Db 89 TGTGTCTGGCGCGCGAGGTGGAAAAATCTAAATCTCTCAAAAAGTAGAGTCGACA 148
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QY 145 TCATAGATGACAACTTTATCTGAGGTGGAAACAGAGCGATGAGTCTGTCGGGAATCTGA 204
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QY 205 CTTTTTCATTCGATTATCAAAAACTGGGATGGATAATTCGATAAAAAATTCGTGGGTGTC 264
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    |||
QY 265 AGAATATTACTAGTACCAATGCAACTTTCTTCACCTCAAGCTGAATGTTTATGAAGAA 324
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Db 269 AGAATATTACTAGTACCAATGCAACTTTCTTCACCTCAAGCTGAATGTTTATGAAGAA 328
    |||
QY 325 TTAATTTGCGTATAGAGCGAAAAAGAAACACTCTTCATGCTATGAGTTCGACTCAT 384
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Db 329 TTAATTTGCGTATAGAGCGAAAAAGAAACACTCTTCATGCTATGAGTTCGACTCAT 388
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QY 385 TTACACCATTTTCGAAAGCTCAGATTGGTCTCTCAGAAAGTACATTTAGAAAGCTGAAGATA 444
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Db 389 TTACACCATTTTCGAAAGCTCAGATTGGTCTCTCAGAAAGTACATTTAGAAAGCTGAAGATA 448
QY 445 AGGCAATAGTGATACACATCTCTCTCGGAACAAAAGATAGTGTATGTGGGCTTTGGATG 504
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Db 449 AGGCAATAGTGATACACATCTCTCTCGGAACAAAAGATAGTGTATGTGGGCTTTGGATG 508
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QY 505 GTTTAAAGCTTTACATATAGCTTACTTATCTGGAAGAAACTCTTCAGGTGTAGAAAGGA 564
    |||
Db 509 GTTTAAAGCTTTACATATAGCTTACTTATCTGGAAGAAACTCTTCAGGTGTAGAAAGGA 568
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QY 565 TTGAAAAATTTATTTCCAGACATAAAATTTATATAACTCTCCAGAGACTTATTGTC 624
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Db 569 TTGAAAAATTTATTTCCAGACATAAAATTTATATAACTCTCCAGAGACTTATTGTC 628
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QY 625 TAAAGTTAAAGCAGCACTACTTACGTCAT-GGAAAAATGGTCTCTATAGTCCAGTACAT 683
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Db 629 TAAAGTTAAAGCAGCACTACTTACGTCCTTTGGAAAAATTTGGTCTCTATAGTCCAGTACAT 688
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QY 684 TGTATTAAGACCACTGTTG-AAATGAACCTTACCTCCACCAGAAAA 727
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Db 689 TGGTTAAAGACCCAGTGTGAAAAATGACTACCTCCCCCGAGAA 733
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RESULT 13
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LOCUS DKFZp781N1092.r1.781 (synonym: hlcc4) Homo sapiens cDNA clone
DEFINITION DKFZp781N1092.5', mRNA sequence.
ACCESSION BX956887
VERSION BX956887.1 GI:43442200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 674)
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
          Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
          Wiemann, S.
TITLE EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
          Wellenreuther, R., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
          MIPS
          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
          This is the 5' sequence of the clone insert
          Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
          Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
          sequenced by DKFZ (German Cancer Research Center.
          Heidelberg/Germany) within the cDNA sequencing consortium of the
          German genome project.
          No sl sequence available.
          This clone (DKFZp781N1092) is available at the RZPD in Berlin.
          Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
          Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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                     /lab_host="DH10B"
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                     /notes="Vector: pSport1_Sfi; Site_1: SfiA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN
Query Match          48.4%; Score 649.4; DB 5; Length 674;
Best Local Similarity 99.4%; Pred. No. 5e-152;
Matches 672; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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361 CTTCAATGATGAGGTTGACTCATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420  
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481 ATAGTGTTATGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAA 540  
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RESULT 14  
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LOCUS  
DEFINITION DKFZp68612447.r1.686 (synonym: hlcc3) Homo sapiens cDNA clone  
ACCESSION DKFZp68612447.5, mRNA sequence.  
VERSION AL707406  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 699)  
Ottewaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and  
Wiemann, S.  
EST (Ottewaelder, B., Obermaier, B., Mewes, H.W., Weil, B. and  
Wiemann, S.)  
JOURNAL Unpublished (2001)  
COMMENT Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Medigenomix (Martinried/Germany) within the cDNA  
sequencing consortium of the German Genome Project. No sl sequence  
available.  
This clone (DKFZp68612447) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
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Db 119 TGCTCGTCGCGGCTCGGGCCATGGGTGTTGTCGCGAGCGCAGGTGGAAAAATCTAAAT 178  
  
Qy 121 CTCTCATAAAAGTAGAGGTGCAATCATAGATGACAACTTTATCTGAGGTGGAAACAGGA 180  
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Db 599 ACTCTTCAGGTGTAGAGAAAGGATTGAAATATTTATTCAGACATATAATTTATAAC 658  
  
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RESULT 15

CD697468 678 bp mRNA linear EST 25-JUN-2003  
LOCUS  
DEFINITION EST13991 human nasopharynx Homo sapiens cDNA, mRNA sequence.

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ACCESSION      CD697468
VERSION        CD697468.1
KEYWORDS       GI:32224985
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
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               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominoidea; Homo.
REFERENCE      1 (bases 1 to 678)
AUTHORS        Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
               Zeng,Y.-X.
TITLE          Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL        Unpublished (2003)
COMMENT        Contact: Yixin Zeng
               Cancer Center
               Sun Yat-sen University
               651 Dongfeng Road East, Guangzhou 510060, China
               Tel: 86-1380-9770-743
               Fax: 86-20-8775-4506
               Email: yxzeng@gzsums.edu.cn.
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FEATURES       source

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## ORIGIN

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Matches 638	Conservative 0	Mismatches 10	Indels 0	Gaps 0
QY	1	CTGCAGCGGATCTGGCGGGCTCCACAGATGATGGTCCTCTCGGGCGCAGCACCCCTAG	60	
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QY	121	CTCTCTCAAAAGTAGAGTGCACATCATAGATGACAACTTTATCCTGAGGTGGACACGGA	180	
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QY	181	GGCATGAGTCTGTCGGGAATGTGACTTTTTCATTTCGATTATCAAAAACTGGGATGATA	240	
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DB	271	ATTGGATAAAATTCCTCGGGGTGCAGATATTACTAGTACCAATGCAACTTTCTTCAC	330	
QY	301	TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGACGAGAAAAAGAAACACTT	360	
DB	331	TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTATAAGACGAGAAAAAGAAACACTT	390	
QY	361	CTTCATCGTATGAGTTGACTCATTTACACCATTTCCGAAGCTCAGTTGGTCTCCAG	420	
DB	391	CTTCATCGTATGAGTTGACTCATTTACACCATTTCCGAAGCTCAGTTGGTCTCCAG	450	
QY	421	AAGTACATTTAGAGCTGAAGATGAAGCAATAGTGATACATCTCTCTGGAAACAAAAG	480	
DB	451	AAGTACATTTAGAGCTGAAGATGAAGCAATAGTGATACATCTCTCTGGAAACAAAAG	510	
QY	481	ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGAAAA	540	
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QY	541	ACTCTTCAGGTGTGAAGAAAGGATTTGAAAATATTTTTCAGACATAAAATTTTATAAC	600	

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2006, 19:25:04 ; Search time 6920 Seconds

(without alignments)  
11031.901 Million cell updates/sec

Title: US-10-824-981-1

Perfect score: 1343  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sta.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1343	100.0	1343	6	A32389 Interferon
3	1343	100.0	1343	6	A76127 Sequence 1
4	1343	100.0	1343	6	AR243657 Sequence
5	1343	100.0	1343	6	AR580340 Sequence
6	1334	99.3	1755	6	A26595 Human inter
7	1334	99.3	1755	6	A32391 Interferon
8	1334	99.3	1755	6	A76129 Sequence 3
9	1334	99.3	1755	6	AR243658 Sequence
10	1334	99.3	1755	6	AR580341 Sequence
11	1330.8	99.1	2755	6	CQ896434 Sequence
12	1330.8	99.1	2755	6	CS118026 Sequence
13	1330.8	99.1	2755	6	AR380573 Sequence
14	1330.8	99.1	2755	8	HUMIFNRA
15	1330.8	99.1	2755	10	G28571 human sts S
16	1330.8	99.1	2784	6	AR030347 Sequence
17	1330.8	99.1	2784	6	I93602 Sequence 1
18	1327.6	98.9	2069	8	AK222770 Homo sapi

19	1326	98.7	2072	8	BC021825	BC021825 Homo sapi
20	1326	98.7	6099	6	CS119636	CS119636 Sequence
21	1324.4	98.6	1968	8	AK222812	AK222812 Homo sapi
22	1318.6	98.2	6741	6	AR491171	AR491171 Sequence
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24	1121.6	83.5	2147	8	AB169002	AB169002 Macaca fa
25	981.2	73.1	1629	6	CQ731750	CQ731750 Sequence
26	824.2	61.4	3230	4	BTIFNAR	X68443 B.taurus IF
27	824.2	61.4	3284	4	BOVIFNRA	L06320 Bos taurus
28	821	61.1	2914	4	OAUF5978	U05978 Ovis aries
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31	625	46.5	4905	4	AF296666	AF296666 Ovis arie
32	540.2	40.2	3894	9	MUSIFNAR	M89641 Mus musculu
33	538.6	40.1	2785	9	BC043935	BC043935 Mus muscu
34	538.6	40.1	3912	9	BC052429	BC052429 Mus muscu
35	537	40.0	3902	9	BC052217	BC052217 Mus muscu
36	251.8	18.7	22936	8	AP000297	AP000297 Homo sapi
37	251.8	18.7	32906	8	HSIFNAR	X60459 Human IFNAR
38	251.8	18.7	35410	8	AY654286	AY654286 Homo sapi
39	251.8	18.7	100000	8	AP000044	AP000044 Homo sapi
40	251.8	18.7	100000	8	AP000112	AP000112 Homo sapi
41	251.8	18.7	100000	8	AP000188	AP000188 Homo sapi
42	251.8	18.7	340000	8	AP001716	AP001716 Homo sapi
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45	224.2	16.7	156045	14	AC144885	AC144885 Papio anu

#### ALIGNMENTS

#### RESULT 1

A26593 LOCUS A26593 1343 bp DNA linear PAT 02-OCT-1995  
DEFINITION Human interferon alpha receptor gene.  
ACCESSION A26593  
VERSION A26593.1 GI:1247458  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1343)  
AUTHORS  
TITLE WATER-SOLUBLE POLYPEPTIDES HAVING HIGH AFFINITY FOR INTERFERONS  
JOURNAL alpha AND beta  
PATENT: WO 9218626-A 17 29-OCT-1992;  
FEATURES  
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#### ORIGIN

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LOCUS Interferon receptor gene.  
DEFINITION A32389  
ACCESSION A32389  
VERSION A32389.1 GI:1567382  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
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AUTHORS .  
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A76127  
LOCUS A76127  
DEFINITION Sequence 1 from Patent WO9320187.  
ACCESSION A76127  
VERSION A76127.1 GI:6088263  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.  
REFERENCE 1 (bases 1 to 1343)  
AUTHORS Benoit, P. and Meyer, F.  
TITLE MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH  
JOURNAL NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON  
Patent: WO 9320187-A 1 14-OCT-1993;  
EUROP BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)  
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RESULT 4  
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DEFINITION Sequence 1 from patent US 6475983.  
ACCESSION AR243657

VERSION AR243657.1 GI:27291031  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1343)  
AUTHORS Bid.P., Gresser,I., Lutfalla,G., Meyer,F., Mogensen,K.E., Tovey,M.  
and Uze,G.  
TITLE Water-soluble polypeptides having a high affinity for .alpha. and  
beta. interferons  
JOURNAL Patent: US 6475983-A 1 05-NOV-2002;  
Medisup International N.V.; Curacao;  
ANX;  
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Best Local Similarity 100.0%; Pred No. 6,1e-290;  
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DEFINITION	Sequence 1 from patent US 6787634.		
ACCESSION	AR580340		
VERSION	AR580340.1	GI:56610636	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1343)		
TITLE	Benoit,P., Meyer,F., Maguire,D., Plavec,I. and Tovey,M.G.		
JOURNAL	Isolated peptide or polypeptide of the extracellular portion of the human interferon receptor (IFN-R)		
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 1755)			
WATER-SOLUBLE POLYPEPTIDES HAVING HIGH AFFINITY FOR INTERFERONS			
alpha AND beta			
Patent: WO 9218626-A 19 29-OCT-1992;			
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Db 1321 GAAATACCTTAAA 1334

## RESULT 7

A32391  
LOCUS 1755 bp DNA linear PAT 08-JUL-1996  
DEFINITION Interferon alpha and beta receptor gene.  
ACCESSION A32391  
VERSION A32391.1 GI:1567384

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo  
1 (bases 1 to 1755)

## REFERENCE

AUTHORS  
JOURNAL  
FEATURES  
source

Patent: FR 2657881-A 20 09-AUG-1991;  
Location/Qualifiers

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Query Match 99.3%; Score 1334; DB 6; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 6.2e-288; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 8

A76129

LOCUS

A76129 1755 bp DNA linear PAT 19-OCT-1999

DEFINITION Sequence 3 from Patent WO9320187.  
ACCESSION A76129  
VERSION A76129.1 GI:6088265  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1755)  
Benoit, P. and Meyer, F.  
AUTHORS MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH  
TITLE NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON  
JOURNAL Patent: WO 9320187-A 3 14-OCT-1993;  
EUROP BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)  
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Query Match 99.3%; Score 1334; DB 6; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 6.2e-288;  
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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LOCUS AR243658  
DEFINITION Sequence 3 from patent US 6475983.  
ACCESSION AR243658  
VERSION AR243658.1 GI:27291032  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1755)  
AUTHORS Eid, P., Greaser, I., Lutfalla, G., Meyer, F., Mogensen, K.E., Tovey, M. and Uze, G.  
TITLE Water-soluble polypeptides having a high affinity for .alpha. and

.beta. interferons	
JOURNAL	Patent: US 6475983-A 3 05-NOV-2002;
ANX;	Medisup International N.V.; Curacao;
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Best Local Similarity 100.0%; Pred. No. 6.2e-288;	
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LOCUS AR580341 1755 bp DNA linear PAT 15-DEC-2004	
DEFINITION Sequence 3 from patent US 6787634.	
ACCESSION AR580341	
VERSION AR580341.1 GI:56610637	
KEYWORDS	
SOURCE Unknown.	
ORGANISM Unknown.	
REFERENCE 1 (bases 1 to 1755)	
AUTHORS Benoit,P., Meyer,F., Maguire,D., Plavec,I. and Tovey,M.G.	
TITLE Isolated peptide or polypeptide of the extracellular portion of the	
human interferon receptor (IFN-R)	
JOURNAL Patent: US 6787634-A 3 07-SEP-2004;	
Medisup International, N.V.; Antilles;	
EPX;	
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Best Local Similarity 100.0%; Pred. No. 6.2e-288;	
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LOCUS CQ896434 2755 bp DNA linear PAT 05-NOV-2004  
DEFINITION Sequence 258 from Patent WO2004076614.  
ACCESSION CQ896434  
VERSION CQ896434.1 GI:55468157  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
MAMMALIA; EUTHERIA; EUARCHONTOGIRES; PRIMATES; CATARTHINI;  
HOMINIDAE; HOMO.  
REFERENCE 1  
AUTHORS Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A., Beckmann, G., Bruemendorf, T., Kimmemann, H., Roepcke, S., Hermann, K., Kinzhong, L., Pillarsky, C. and Staub, E.  
TITLE Human nucleic acid sequences obtained from prostatic carcinomas  
JOURNAL Patent: WO 2004076614-A 258 10-SEP-2004;  
Hinzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE); Specht, Thomas (DE); Schmitt, Armin (DE)  
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Query Match 99.1%; Score 1330.8; DB 6; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 3.2e-287;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTGCGGAGATCTGCGCGGCTCCAGATGATGGTCTCTCTGCGCGGCGAGACCTAG 60  
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CS118026

LOCUS CS118026 2755 bp DNA linear PAR 08-JUL-2005

DEFINITION Sequence 73 from Patent WO2005054508.

ACCESSION CS118026

VERSION CS118026.1 GI:70665972

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D. and Debono,S.

TITLE Gene expression profiling of colon cancer by dna microarrays and correlation with survival and histoclinical parameters

JOURNAL Patent: WO 2005054508-A 73 16-JUN-2005; Ipoogen (FR); Institut Paoli-Calmettes, Ipc (FR); Institut National de la Sante et de la Recherche Medicale (INSERM) (FR)

FEATURES

Location/Qualifiers

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/organism="synthetic construct"

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/notes="Description of Artificial sequences:primer"

misc\_feature 1..2755

/notes="interferon (alpha, beta and omega) receptor 1(IFNAR1) gene."

ORIGIN

Query Match 99.1%; Score 1330.8; DB 6; Length 2755;

Best Local Similarity 99.9%; Pred. No. 3.2e-287;

Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCAGGGATCTGGCGGGCTCCAGATGATGGTCCTCTCGGGCGGACGACCTAG 60

Db 53 CTGGTGGGATCTGGCGGGCTCCAGATGATGGTCCTCTCGGGCGGACGACCTAG 112

Qy 61 TGCTCGTCCGCTGGCGCCATGGGTGTTGTCGCGAGCGCGAGGTGGA AAAATCTAAAT 120

Db 113 TGCTCGTCCGCTGGCGCCATGGGTGTTGTCGCGAGCGCGAGGTGGA AAAATCTAAAT 172

Qy 121 CTCCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTGAGGTGGAAACAGGA 180

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Qy 181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTTCAAAAACCTGGGATGGATA 240

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Db 773 CAGAAAAATATAGAGTCTAGTGTCCAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 832

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DEFINITION	Sequence 1118 from patent US 6607879.	linear	PAT 18-DEC-2003
ACCESSION	AR380573		
VERSION	AR380573.1	GI:40088207	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2755)		
AUTHORS	Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.		
TITLE	Compositions for the detection of blood cell and immunological		
JOURNAL	response gene expression		
PATENT	US 6607879-A 1118 19-AUG-2003;		
INCYTE	Incyte Corporation; Palo Alto, CA		
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Query Match 99.1%; Score 1330.8; DB 6; Length 2755;			
Best Local Similarity 99.9%; Pred. No. 3.2e-287;			
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Qy	961	GAAATAACACATCTTTTGTGCTGAAGAGATAAGTTTGTATCTGAAATACAAAGCTTTCC	1020
Db	1013	GAAATAACACATCTTTTGTGCTGAAGAGATAAGTTTGTATCTGAAATACAAAGCTTTCC	1072
Qy	1021	TACTTCTCCAGTCTTTAAACATTTAGATCCCTTACTGTGATTCATTTCCATATCTATATCCGGTG	1080
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RESULT 14  
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LOCUS HUMIFNRA 2755 bp mRNA linear PRI 08-NOV-1994  
DEFINITION Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds.  
ACCESSION J03171  
VERSION J03171.1 GI:184645  
KEYWORDS interferon-alpha receptor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2755)  
AUTHORS Uze, G., Lutfalla, G. and Gresser, I.  
TITLE Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA  
JOURNAL Cell 60 (2), 225-234 (1990)  
PUBMED 2153461  
COMMENT Original source text: Human cell line DAUDI, cDNA to mRNA.  
Draft entry and computer-readable sequence for [1] kindly submitted by G.Uze, 29-NOV-1989, for release after publication.

FEATURES  
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ORIGIN  
Query Match 99.1%; Score 1330.8; DB 8; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 3 2e-287;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CTGCAGGATCTGGCGGCTCCAGATGATGGTGTCTCTCGGCGCAGACCCCTAG 60  
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Db 53 CTGCTGGGATCTGGCGGCTCCAGATGATGGTGTCTCTCTGGCGCGACGCCCTAG 112  
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## RESULT 15

G28571 LOCUS human STS SHGC-35315, 2755 bp DNA linear STS 11-JUL-1996

DEFINITION G28571 human STS SHGC-35315, sequence tagged site.

VERSION G28571.1 GI:1408386

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2755)  
Myers,R.M.  
Unpublished (1996)

## REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu

Primer A: TGACAGAAATGAAGCTGTGCA

Primer B: TTTAAATAGTTAAGAGCTTGCCCG

STS size: 175

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

## Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

## Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from J03171

-- Washington University/Merck EST sequence.

## FEATURES

## source

1..2755

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/map="21"  
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ORIGIN

Query Match 99.1%; Score 1330.8; DB 10; Length 2755;  
Best Local Similarity 99.9%; Pred. No. 3.2e-287;  
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Qy	1201	CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACACCATGG	1260
Db	1253	CAGTTCCTTAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGACACACCATGG	1312
Qy	1261	ATGAAAAGCTGAATAAAGCAGTGTGTTTTAGTGAAGCTGTATGTGAGAAAAACAAACCAG	1320
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Qy	1321	GAATACCTCTAAA	1334
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GenCore version 5.1.6  
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## SUMMARIES

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5	1334	99.3	1755	3	US-07-971-834-3
6	1334	99.3	1755	3	US-09-240-675-3
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27	38.6	2.9	1959	3	US-09-377-466B-3	Sequence 3, Appl
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29	38.6	2.9	2430	6	PCT-US92-00040-1	Sequence 1, Appl
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## ALIGNMENTS

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; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1343 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

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RESULT 2
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; Sequence 1, Application US/07971834
; Patent No. 6475983
; GENERAL INFORMATION:
; APPLICANT: EID, Pierre
; APPLICANT: GRESSER, Ion
; APPLICANT: LUTFALLA, Georges
; APPLICANT: MEYER, Francois
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: TOVEY, Michael
; APPLICANT: UZE, Gilles
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH
; AFFINITY FOR INTERFERONS ALPHA AND BETA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/07/971,834
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00318
; FILING DATE: 17-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 27..1334
US-07-971-834-1

Query Match      100.0%; Score 1343; DB 3; Length 1343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAGGAGTCTGGCGGCTCCAGATGATGGTGGTCTCTCTGGGCGGCGAGCCCTAG 60
Db 1 CTGCAGGAGTCTGGCGGCTCCAGATGATGGTGGTCTCTCTGGGCGGCGAGCCCTAG 60

Qy 61 TGCTCGTGGCGTGGCGCCCATGGGTGTGTCGCGAGCGGAGGTGGAAAAATCTAAAT 120
Db 61 TGCTCGTGGCGTGGCGCCCATGGGTGTGTCGCGAGCGGAGGTGGAAAAATCTAAAT 120

Qy 121 CTCTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGGAACAGGA 180
Db 121 CTCTCTCAAAAAGTAGAGTGCACATCATAGATGACAACTTTATCTGAGGTGGGAACAGGA 180

Qy 181 GCGATGAGTCTGCGGGAATGTACTTTTCATTCGATATCAAAAAAATCGGATGGATA 240
Db 181 GCGATGAGTCTGCGGGAATGTACTTTTCATTCGATATCAAAAAAATCGGATGGATA 240

Qy 241 ATTGGATAAAATTTCTGGGTGTGAGATATTAATCTAGTACCAATGCACTTTCTTCAC 300
Db 241 ATTGGATAAAATTTCTGGGTGTGAGATATTAATCTAGTACCAATGCACTTTCTTCAC 300

Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATAAGAGCAGAAAAACAACTT 360
Db 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATAAGAGCAGAAAAACAACTT 360

Qy 361 CTTCATGATGAGGTTGACTCATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420
Db 361 CTTCATGATGAGGTTGACTCATTTACACCAATTCGCAAGCTCAGATTGGTCTCCAG 420

Qy 421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTATGATACATCTCTCTCGGAACAAAG 480
Db 421 AAGTACATTTAGAGCTGAAGATAGGCAATAGTATGATACATCTCTCTCGGAACAAAG 480

Qy 481 ATAGTGTATGCGGCTTTGGATGTTTAAGCTTTACATATAGCTTACTTATCTGGAATA 540
Db 481 ATAGTGTATGCGGCTTTGGATGTTTAAGCTTTACATATAGCTTACTTATCTGGAATA 540

Qy 541 ACTCTTCAGGTGTAGAGAAAGGATTTGAAAAATTTTATTCAGACATAAAATTTATAAC 600
Db 541 ACTCTTCAGGTGTAGAGAAAGGATTTGAAAAATTTTATTCAGACATAAAATTTATAAC 600

Qy 601 TCTCAGCAGACTACTTATTTGTCTAAAGTTAAAGCAGCACTACTTACGTCTAGTGAATA 660
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Qy 661 TTGGTGTCTAGTCCAGTACATTTGTATTAAGACCAAGTTGAAATGAACCTACTCCAC 720
Db 661 TTGGTGTCTAGTCCAGTACATTTGTATTAAGACCAAGTTGAAATGAACCTACTCCAC 720

Qy 721 CAGAAAAATATAGAAAGTCTAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780
Db 721 CAGAAAAATATAGAAAGTCTAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780

Qy 781 ATGCAAAATGACCTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAAAGGAATCTCGAA 840
Db 781 ATGCAAAATGACCTTTCAAGTTCAGTGGCTCCAGCCTTTTAAAAAGGAATCTCGAA 840

Qy 841 ACCATTTGTATTAATGGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900
Db 841 ACCATTTGTATTAATGGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900
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## RESULT 3

US-09-240-675-1

; Sequence 1, Application US/09240675

; Patent No. 6787634

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick

; APPLICANT: MEYER, Francois

; APPLICANT: MAGUIRE, Deborah

; APPLICANT: PLAVEC, Ivan

; APPLICANT: TOVEY, Michael G.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley &amp; Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/240,675

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/307,588

; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: PCI/EP93/00770

; FILING DATE: 30-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 92400902.0

; FILING DATE: 31-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: SAXE, Bernhard D.



```
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1755 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 27..1697
; US-08-307-588-3

Query Match 99.3%; Score 1334; DB 2; Length 1755;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCGAGGATCTGCGCGGCTCCAGATGATGTCCTCTCGGCGCGAGCACCCTAG 60
Db 1 CTGCGAGGATCTGCGCGGCTCCAGATGATGTCCTCTCGGCGCGAGCACCCTAG 60
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Db 121 CTCCTCAAAAAGTAGAGGTGCAATCATAGATGCACTTTATCTGAGGTGGAACAGGA 180
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Db 181 GCGATGATCTGCGGAAATGTCGAGATATTTCTGATGATTAATCAAAAAGTGGATGATA 240
Qy 241 ATTGGATAAATGTCGCGGCTGAGATATTTCTGATGATTAATCAAAAAGTGGATGATA 300
Db 241 ATTGGATAAATGTCGCGGCTGAGATATTTCTGATGATTAATCAAAAAGTGGATGATA 300
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTAAGAGCAGAGAAAGAAACACTT 360
Db 301 TCAAGCTGAATGTTTATGAAGAAATTAATTCGCTAAGAGCAGAGAAAGAAACACTT 360
Qy 361 CTTCAATGATGAGGTGACTCATTTACCAATTTGCAAAAGCTCAGATTCCTCCAG 420
Db 361 CTTCAATGATGAGGTGACTCATTTACCAATTTGCAAAAGCTCAGATTCCTCCAG 420
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Db 421 AAGTACATTTAGAGCTGAAGTGAAGCAATGATGATACATCTCTCTCGGAAACAAAG 480
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Db 481 ATAGTGTATGTCGCTTTGATGTTTAAAGCTTTTACATATAGCTTACTTATCTGAAA 540
Qy 541 ACTCTTCAGGTGTAAGAAAGAGTGAATAATTTATTCAGACATATAATTTATAAAC 600
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Db 781 ATGCAAAATGAGTGTCTCAAGTTCAGTGGTCCAGCGCTTTTAAAGAGGAATCCTGAA 840
Qy 841 ACCATTTGATTAATGAAACAAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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Db 961 GAAATAACACATCTTTTGGTCTGAGAGATAAAGTTGATCTGAAATACAAAGCTTTCC 1020
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Db 1081 CTCCAAACACATCTGGAACACACGCTGTGATCCAGGATTTATCCATGATTTATGAAATTA 1140
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Qy 1201 CAGTTCCTTAATTTGAAACCACTGCTGATTTATGTTGTTGTTGTTGTTGTTGTTGTTG 1260
Db 1201 CAGTTCCTTAATTTGAAACCACTGCTGATTTATGTTGTTGTTGTTGTTGTTGTTGTTG 1260
Qy 1261 ATGAAAAGCTGAAATAAAGCAGTCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db 1261 ATGAAAAGCTGAAATAAAGCAGTCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Qy 1321 GAAATACCTCTAAA 1334
Db 1321 GAAATACCTCTAAA 1334

RESULT 5
US-07-971-834-3
; Sequence 3, Application US/07971834
; Patent No. 6475983
; GENERAL INFORMATION:
; APPLICANT: BID, Pierre
; APPLICANT: GRESSER, Ion
; APPLICANT: LUTFALLA, Georges
; APPLICANT: MEYER, Francois
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: TOVEY, Michael
; APPLICANT: UZE, Gilles
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH
; TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/07/971,834
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/FR91/00318
; APPLICATION NUMBER: 17-APR-1991
; FILING DATE: 17-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: BID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1755 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 27..1697
; US-07-971-834-3

Query Match 99.3%; Score 1334; DB 3; Length 1755;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGGATCTGCGGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 60
DB 1 CTGAGGGATCTGCGGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 60

QY 61 TGCTGTCGCGGTGGGCCATGGTGTGTCGCGAGCCGAGGTGGAAAAATCTAAAT 120
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QY 241 ATTGGATAAAATGTCTGGGTGTCAGAAATTAATAGTACCAATGCAACTTTTCTTTCAC 300
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QY 301 TCAAGCTGAATGTTATGAAGAAATTAATTAATGCGTATAGAGCAGAGAAAGAAACACTT 360
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DB 421 AAGTACATTTAGAGCTGGAAGTAAGCAATAGTATACATCTCTCTGGAAACAAAG 480

QY 481 ATAGTGTATGCGGCTTGGATGGTTTAAAGCTTACATATAGCTTACTTATCTGAAAA 540
DB 481 ATAGTGTATGCGGCTTGGATGGTTTAAAGCTTACATATAGCTTACTTATCTGAAAA 540

QY 541 ACTCTTCAGTGTAGAGAAAGGATGAAAAATTTTATTCAGACATATAAAATTTATAAC 600
DB 541 ACTCTTCAGTGTAGAGAAAGGATGAAAAATTTTATTCAGACATATAAAATTTATAAC 600

QY 601 TCTCACAGAGACTACTTATGCTTAAAGTTAAAGCAGCAGCTACTTACGTCATGAAAA 660
DB 601 TCTCACAGAGACTACTTATGCTTAAAGTTAAAGCAGCAGCTACTTACGTCATGAAAA 660
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DB 661 TTGGTGTCTATAGTCCAGTACATTTATATAAGACCACAGTTGAAAAATGAACCTACCTCCAC 720

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QY 841 ACCATTGTATAAATGAAAAACAAATACCTGACGTGAAAAATGTCAAAACTACCCAGGTG 900
DB 841 ACCATTGTATAAATGAAAAACAAATACCTGACGTGAAAAATGTCAAAACTACCCAGGTG 900

QY 901 TCTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTCATG 960
DB 901 TCTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTCATG 960

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DB 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATCAAGCTTTCC 1020

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QY 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTAAGCCAGAGCACACACCATGG 1260
DB 1201 CAGTTCCTTAATTTGAAACCACTGACTGTATATTGTGTAAGCCAGAGCACACACCATGG 1260

QY 1261 ATGAAAGCTGAAATAAAGCAGTGTGTTTGTAGTCGCGCTGTATGTGAGAAAAACAAACAG 1320
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QY 1321 GAAATACCTCTAAA 1334
DB 1321 GAAATACCTCTAAA 1334
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RESULT 6
US-09-240-675-3
; Sequence 3, Application US/09240675
; Patent No. 6787634
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,675  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/307,588  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1755 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 27..1697  
US-09-240-675-3

Query Match 99.3%; Score 1334; DB 3; Length 1755;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTGCAGGAGTCTGGCGGCTCCAGATGATGGTCTCTCTGGGCGCAGACCCCTAG 60
Db 1 CTGCAGGAGTCTGGCGGCTCCAGATGATGGTCTCTCTGGGCGCAGACCCCTAG 60
Qy 61 TGCTCGTCGCGCGGCCCATGGTGTTCGCGAGCGCGAGGTGGAAAAATCTAAAT 120
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Qy 361 CTTCAATGATGAGGTGACTCATTTACACATTTCCGAAAGCTCAGATTCCTCCAG 420
Db 361 CTTCAATGATGAGGTGACTCATTTACACATTTCCGAAAGCTCAGATTCCTCCAG 420
Qy 421 AAGTACATTTAGAAGCTCAAGTAAGCAATAGTATACATCTCTCTCGAACCAAG 480
Db 421 AAGTACATTTAGAAGCTCAAGTAAGCAATAGTATACATCTCTCTCGAACCAAG 480
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Qy 721 CAGAAAAATATAGAGTCTAGTCTCAAAATCAGAACTATGTTCTTTAAATGGGATTATACAT 780
Db 721 CAGAAAAATATAGAGTCTAGTCTCAAAATCAGAACTATGTTCTTTAAATGGGATTATACAT 780
Qy 781 ATGCAAAACATGACCTTTCAAGTTCAGTGGTCTCAGCGCTTTTAAAGAAATCCTTGAA 840
Db 781 ATGCAAAACATGACCTTTCAAGTTCAGTGGTCTCAGCGCTTTTAAAGAAATCCTTGAA 840
Qy 841 ACCATTTGTATAATGGAACAAATACCTGACTGTGAAAAATGTCAAACTACCCAGTGTG 900
Db 841 ACCATTTGTATAATGGAACAAATACCTGACTGTGAAAAATGTCAAACTACCCAGTGTG 900
Qy 901 TCTTTCTCAAAACGTTTTCCAAAAAGAAATTTACCTTCTCCGCTCAAGCACTCTGATG 960
Db 901 TCTTTCTCAAAACGTTTTCCAAAAAGAAATTTACCTTCTCCGCTCAAGCACTCTGATG 960
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Db 1021 TACTTCTCAGTCTTTAAACATTTAGATCCCTTAGTATTCATTCATATCTATATCGGTG 1080
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Db 1081 CTCCAAAAACAGTCTGGAACACAGCGCTGTGATCCAGGATTTCCACTGATTTATGAAATTA 1140
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Qy 1261 ATGAAAGCTCAATAAAGCAGTGTGTTTGTAGTACGCTGTATGTGAGAAAAACAAACCAG 1320
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Qy 1321 GAAATACCTCTAAA 1334
Db 1321 GAAATACCTCTAAA 1334
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## RESULT 7

US-09-023-655-1118

; Sequence 1118, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; NUMBER OF INVENTION: EXPRESSION

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2755 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g184645  
US-09-023-655-1118

Query Match 99.1%; Score 1330.8; DB 3; Length 2755;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCGAGGATCTCGGCGGCTCCAGATGATGTCCTCTCGGCGGCGAGCCTTAG 60  
DB 53 CTGCTGGGATCTCGGCGGCTCCAGATGATGTCCTCTCGGCGGCGAGCCTTAG 112  
QY 61 TGCTCGTGGCGGTCGATGGTGTTCGCGAGCGGAGGTGGAAAAATCTAAAT 120  
DB 113 TGCTCGTGGCGGTCGATGGTGTTCGCGAGCGGAGGTGGAAAAATCTAAAT 172  
QY 121 CTCTCAAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 180  
DB 173 CTCTCAAAAAGTAGAGTGCATCATAGATGACAACTTTATCTCGAGTGGAAACAGGA 232  
QY 181 GCGATGAGTCTGCGGGAATGTGACTTTTTCATTTCGATTATCAAAAACCTGGGATGGATA 240  
DB 233 GCGATGAGTCTGCGGGAATGTGACTTTTTCATTTCGATTATCAAAAACCTGGGATGGATA 292  
QY 241 ATTGGATAAATTTGCTGGGTGTGAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 300  
DB 293 ATTGGATAAATTTGCTGGGTGTGAGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 352  
QY 301 TCAAGCTGAATGTTTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360  
DB 353 TCAAGCTGAATGTTTGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412  
QY 361 CTTTCATGATGAGTGTGACTCAATTTACACATTTTCGAAAGCTCAGATTTGGTCTCCAG 420  
DB 413 CTTTCATGATGAGTGTGACTCAATTTACACATTTTCGAAAGCTCAGATTTGGTCTCCAG 472  
QY 421 AAGTACATTTAGAGCTGAAGAAAGGCAATAGTATACATCTCTCTCTGGAAACAAAAG 480  
DB 473 AAGTACATTTAGAGCTGAAGAAAGGCAATAGTATACATCTCTCTCTGGAAACAAAAG 532  
QY 481 ATAGTGTATGTCGGCTTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 540  
DB 533 ATAGTGTATGTCGGCTTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 592  
QY 541 ACTCTTCAGGTGTAGAAGAAAGGATTTGAAATATTTTATTCAGACATAAAATTTATAAAC 600

DB 593 ACTCTTCAGGTGTAGAAGAAAGGATTTGAAATATTTTATTCAGACATAAAATTTATAAAC 652  
QY 601 TCTCACCAGAGTACTTATTTCTTAAAGTTTAAAGCAGCAGTACTTACGTCTATGGAAA 660  
DB 653 TCTCACCAGAGTACTTATTTCTTAAAGTTTAAAGCAGCAGTACTTACGTCTATGGAAA 712  
QY 661 TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAACAGTTGAAATGAATGAATGAATGAAT 720  
DB 713 TTGGTGTCTATAGTCCAGTACATTTGATATAAGACCAACAGTTGAAATGAATGAATGAATGAAT 772  
QY 721 CAGAAAATATAGAAGTCAAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780  
DB 773 CAGAAAATATAGAAGTCAAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 832  
QY 781 ATGCAAAATGACCTTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 840  
DB 833 ATGCAAAATGACCTTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG 892  
QY 841 ACCATTTGATATAAGTCAAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 900  
DB 893 ACCATTTGATATAAGTCAAGTCTCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 952  
QY 901 TCTTTCTCAAAACGTTTTCCTCAAAAGGAAATTTACCTTCTCCGCGTACAGCATCTGATG 960  
DB 953 TCTTTCTCAAAACGTTTTCCTCAAAAGGAAATTTACCTTCTCCGCGTACAGCATCTGATG 1012  
QY 961 GAAATAACACATCTTTTCTGCTGAAGAGATAAAGTTTGAATCTGAAATCAAGATTTTCC 1020  
DB 1013 GAAATAACACATCTTTTCTGCTGAAGAGATAAAGTTTGAATCTGAAATCAAGATTTTCC 1072  
QY 1021 TACTTCTCCAGTCTTTTAAATTTAGATCCTTTAGTATTCATTTCATATCTATATCGGTG 1080  
DB 1073 TACTTCTCCAGTCTTTTAAATTTAGATCCTTTAGTATTCATTTCATATCTATATCGGTG 1132  
QY 1081 CTCCAAAACAGTCTGGAACACGCTGTGATCCAGGATTTACCTGATTTATGAATTA 1140  
DB 1133 CTCCAAAACAGTCTGGAACACGCTGTGATCCAGGATTTACCTGATTTATGAATTA 1192  
QY 1141 TTTTGGGAAACACATTTCAATGCTGAGAGAAATTTATCGAGAAACCTGATGTTA 1200  
DB 1193 TTTTGGGAAACACATTTCAATGCTGAGAGAAATTTATCGAGAAACCTGATGTTA 1252  
QY 1201 CAGTCTCAATTTGAAACCACTGATGATATTTGTTGAAAGCCAGACACACCATGG 1260  
DB 1253 CAGTCTCAATTTGAAACCACTGATGATATTTGTTGAAAGCCAGACACACCATGG 1312  
QY 1261 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGAACCTGTATGTGAGAAACCAAAACCAG 1320  
DB 1313 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGAACCTGTATGTGAGAAACCAAAACCAG 1372  
QY 1321 GAAATACCTCTAAA 1334  
DB 1373 GAAATACCTCTAAA 1386

RESULT 8

US-09-949-016-101  
; Sequence 101, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE OF INVENTION: CL001307  
; FILE REFERENCE: US/09/949,016  
; CURRENT APPLICATION NUMBER: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 2755
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-101

Query Match      99.1%; Score 1330.8; DB 3; Length 2755;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTG CAGGAGTCTGCGGGGCTCCAGATGATGGTCTCTCTGCGGCGGACGCCCTAG 60
Db |||
Qy 53 CTGGTGGGATCTGGGGGCTCCAGATGATGGTCTCTCTGCGGCGGACGCCCTAG 112
Db |||
Qy 61 TGCTCGTGGCGTGGGCGGCTGGGCTGGTCCGAGCGCGGAGGTGGAAAAATCTAAAT 120
Db |||
Qy 113 TGCTCGTGGCGTGGGCGGCTGGGCTGGTCCGAGCGCGGAGGTGGAAAAATCTAAAT 172
Db |||
Qy 121 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACACTTTTCAATCGATTATCAAAAACCTGGATGATA 240
Db |||
Qy 173 CTCCTCAAAAAGTAGAGTGCACATCATAGATGACACTTTTCAATCGATTATCAAAAACCTGGATGATA 232
Db |||
Qy 181 GCGATGAGTCTGCGGGAATGACTTTTCAATCGATTATCAAAAACCTGGATGATA 240
Db |||
Qy 233 GCGATGAGTCTGCGGGAATGACTTTTCAATCGATTATCAAAAACCTGGATGATA 292
Db |||
Qy 241 ATTGCGATAAAATGCTCGGGGTGTCAGATAATTAATCTAGTACCAAAATGCAACTTTTCTTCAC 300
Db |||
Qy 293 ATTGCGATAAAATGCTCGGGGTGTCAGATAATTAATCTAGTACCAAAATGCAACTTTTCTTCAC 352
Db |||
Qy 301 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 360
Db |||
Qy 353 TCAAGCTGAATGTTTATGAAGAAATTAATTTGCGTATAGAGCAGAAAAAGAAACACTT 412
Db |||
Qy 361 CTTCAATGATAGAGTTCAGTCACTTATACACATTCGCAAGCTCAGATTGGTCTCCAG 420
Db |||
Qy 413 CTTCAATGATAGAGTTCAGTCACTTATACACATTCGCAAGCTCAGATTGGTCTCCAG 472
Db |||
Qy 421 AAGTACATTTAGAGCTCAAGATAGGCAATAGTATGATACACATCTCTCTCGAAACAAAG 480
Db |||
Qy 473 AAGTACATTTAGAGCTCAAGATAGGCAATAGTATGATACACATCTCTCTCGAAACAAAG 532
Db |||
Qy 481 ATAGTGTATGCGGCTTTGGATGGTTAAGCTTTTACATATAGCTTACTTATCTGGAAAA 540
Db |||
Qy 533 ATAGTGTATGCGGCTTTGGATGGTTAAGCTTTTACATATAGCTTACTTATCTGGAAAA 592
Db |||
Qy 541 ACTCTTCAGGTGTAGAGAAAGGATGAAATATTTATTCAGACATATAAAATTTATAAAC 600
Db |||
Qy 593 ACTCTTCAGGTGTAGAGAAAGGATGAAATATTTATTCAGACATATAAAATTTATAAAC 652
Db |||
Qy 601 TCTCAGCAGACTACTTATTTCTTAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 660
Db |||
Qy 653 TCTCAGCAGACTACTTATTTCTTAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 712
Db |||
Qy 661 TTGGTGTCTATAGTTCAGTACATTTGTATAAAGCAGCACTGTTGAAATGAACTCTCCAC 720
Db |||
Qy 713 TTGGTGTCTATAGTTCAGTACATTTGTATAAAGCAGCACTGTTGAAATGAACTCTCCAC 772
Db |||
Qy 721 CAGAAAAATATAGAGTTCAGTTCAGAAATCAGAACTATGTTCTTAAATGGGATATACAT 780
Db |||
Qy 773 CAGAAAAATATAGAGTTCAGTTCAGAAATCAGAACTATGTTCTTAAATGGGATATACAT 832
Db |||
Qy 781 ATGAAAAATATAGAGTTCAGTTCAGTTCAGAAATCAGAACTATGTTCTTAAATGGGATATACAT 840
Db |||
Qy 833 ATGAAAAATATAGAGTTCAGTTCAGTTCAGAAATCAGAACTATGTTCTTAAATGGGATATACAT 892
Db |||
Qy 841 ACCATTTGTATAAATGGGAAACAAATACCTGCTGAAATGTCAAACTACCCAGTGTG 900
Db |||
Qy 893 ACCATTTGTATAAATGGGAAACAAATACCTGCTGAAATGTCAAACTACCCAGTGTG 952
Db |||
Qy 901 TCTTTCTCAAAACGTTTTTCAAAAGGAAATTTACCTTTCTCCGCGTACAAGCATCTGATG 960
Db |||

; RESULT 9
; US-08-471-454-1
; Sequence 1, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
```





TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2784 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-466-974-1

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Query Match      99.1%; Score 1330.8; DB 2; Length 2784;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0;
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Matches	1332;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	CTGCAGGGATCTGCGGGCTCC	CAGATGATGGT	CGTCTCTCGGGCGCGACGACCC	TAG	60			
Db	53	CTGGTGGGATCTGCGGGCTCC	CAGATGATGGT	CGTCTCTCGGGCGCGACGACCC	TAG	112			
Qy	61	TGCTCTGCGGGTGGGCCCCAT	TGGGTGTTC	CGCAGCGCGAGGTGGAAAAAT	CTAAAT	120			
Db	113	TGCTCTGCGGGTGGGCCCCAT	TGGGTGTTC	CGCAGCGCGAGGTGGAAAAAT	CTAAAT	172			
Qy	121	CTCTCAAAAAGTAGAGGTGC	ACATCATAGATGACAACTT	TATCTCGAGGTGGACAGGA	180				
Db	173	CTCTCAAAAAGTAGAGGTGC	ACATCATAGATGACAACTT	TATCTCGAGGTGGACAGGA	232				
Qy	181	GCGATGAGTCTGTCGGGAAT	TGACTTTTTT	CATTTCGATTAACAAAAAT	CTGGATGGATA	240			
Db	233	GCGATGAGTCTGTCGGGAAT	TGACTTTTTT	CATTTCGATTAACAAAAAT	CTGGATGGATA	292			
Qy	241	ATTGGATAAAATTGCTCTGG	TGTCAGAAATATTA	CTAGTACCAAATGCAACTTTT	CTTCAC	300			
Db	293	ATTGGATAAAATTGCTCTGG	TGTCAGAAATATTA	CTAGTACCAAATGCAACTTTT	CTTCAC	352			
Qy	301	TCAAGCTGAATGTTTATGA	AGAAATTAATTTGCGTATA	TAAGNAGCAGAAAAAGAACACTT	360				
Db	353	TCAAGCTGAATGTTTATGA	AGAAATTAATTTGCGTATA	TAAGNAGCAGAAAAAGAACACTT	412				
Qy	361	CTTTCATGGTATGAGTTTG	ACTCATTTTACACCAATTT	CGCAAGCTCAGATTCGTCTCC	CCAG	420			
Db	413	CTTTCATGGTATGAGTTTG	ACTCATTTTACACCAATTT	CGCAAGCTCAGATTCGTCTCC	CCAG	472			
Qy	421	AAGTACATTTAGAGCTGA	AGATTAAGCAATAGTGATA	CACATCTCTCTGGAACAAAG	480				
Db	473	AAGTACATTTAGAGCTGA	AGATTAAGCAATAGTGATA	CACATCTCTCTGGAACAAAG	532				
Qy	481	ATAGTGTATTGCGGCTTT	TGATGGTTTTAGCTTTT	AAGCTTTACATATAGCTT	ATCTGGAATA	540			
Db	533	ATAGTGTATTGCGGCTTT	TGATGGTTTTAGCTTTT	AAGCTTTACATATAGCTT	ATCTGGAATA	592			
Qy	541	ACTCTTCAGGTGTAGAG	AAAGGATTCGAAATATTT	ATTCAGACATATAAATTTT	ATAAC	600			
Db	593	ACTCTTCAGGTGTAGAG	AAAGGATTCGAAATATTT	ATTCAGACATATAAATTTT	ATAAC	652			
Qy	601	TCTCACACAGAGACTACT	TATTTGCTCTAAAAGTT	TAAGCAGCACTACTTACGT	CATGGAATA	660			
Db	653	TCTCACACAGAGACTACT	TATTTGCTCTAAAAGTT	TAAGCAGCACTACTTACGT	CATGGAATA	712			
Qy	661	TTGGTGTCTATPAGTCC	AGTACATTTGTATAAAG	CCACAGTTGAAAAATGAACT	CTCCAC	720			
Db	713	TTGGTGTCTATPAGTCC	AGTACATTTGTATAAAG	CCACAGTTGAAAAATGAACT	CTCCAC	772			
Qy	721	CAGAAATATAGAAGTCA	GTGTCCAAATCAGAACT	ATGTTCTTTAAATGGGATTA	TATCAT	780			
Db	773	CAGAAATATAGAAGTCA	GTGTCCAAATCAGAACT	ATGTTCTTTAAATGGGATTA	TATCAT	832			
Qy	781	ATGCACAACATGACCTTT	CAAGTTCAGTGGCTCC	ACGGCTTTTAAAAGGAAT	CTTGAA	840			
Db	833	ATGCACAACATGACCTTT	CAAGTTCAGTGGCTCC	ACGGCTTTTAAAAGGAAT	CTTGAA	892			
Qy	841	ACCATTTGTTATAAATG	GAACAAATACCTGACT	GTGAAAAATGTCAAACT	ATCACCAGTGTG	900			

[illegible]

## RESULT 11

US-08-471-453-1  
; Sequence 1, Application US/08471453  
; Patent No. 5886153

FACEBOOK NO: 3886153  
GENERAL INFORMATION:

APPLICANT: MOGENSEN. Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LUTFALLA, Georges

APPLICANT: GRESSER, Ion

**TITLE OF INVENTION:** CDNA FRAGMENT

THE ALPH

PREPARATION	TITLE OF INVENTION:

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERH

STREET: 1100 NORTH GLEBE RD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
;

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;
;COMPUTER: IBM PC compatible
;COMPUTER: IBM PC compatible
;COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/M

SOFTWARE: Patent In Release  
CURRENT APPLICATION DATA:

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER. IUS/08/

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APPLICATION NUMBER: US/08/  
FILING DATE: 05-JUN-1995

FILING DATE: 06-JUN-1995  
CLASSIFICATION: 536

CLASSIFICATION: 536  
PRIOR APPLICATION DATA.

; PRIOR APPLICATION DATA:  
 . APPLICATION NUMBER: IIS 07/

APPLICATION NUMBER: US 077  
FILING DATE: 15-JUN-1992

FILING DATE: 13-JUN-1992  
APPLICATION NUMBER: FR 89/

DECLASSIFICATION NUMBER: FK 857  
FILING DATE: 20-OCT-1989

FILED DATE: 20-OCT-1989  
ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

NAME: DAVIS, THOMAS E.  
REGISTRATION NUMBER: 32,200

```
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2784 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-471-453-1

Query Match      99.1%; Score 1330.8; DB 2; Length 2784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCAGGGATCTGGCGGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 60
DB 53 CTGGTGGGATCTGGCGGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 112
QY 61 TGCTCTGGCGGGTGGGCGGATGGTGTGTCGGAGCGGAGGTGGAAAAATCTAAAT 120
DB 113 TGCTCTGGCGGGTGGGCGGATGGTGTGTCGGAGCGGAGGTGGAAAAATCTAAAT 172
QY 121 CTCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTCGAGGTGGAAACAGGA 180
DB 173 CTCTCAAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTCGAGGTGGAAACAGGA 232
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DB 233 GCGATGAGTCTGTGGGAAATGTGACTTTTTCATTTCGATTATCAAAAACTGGGATGGATA 292
QY 241 ATTGGATAAAATTTCTCGGGTGTGAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC 300
DB 293 ATTGGATAAAATTTCTCGGGTGTGAGAAATATTACTAGTACCAATGCAACTTTTCTTCAC 352
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DB 353 TCAAGCTGAATGTTTATGAGAAATTAATTTGGTATTAAGAGCAGAAAGAAACACTT 412
QY 361 CTTTCATGATGAGGTGACTCATTTACACCAATTTCCAAAGCTCAGATTGGTCTCCAG 420
DB 413 CTTTCATGATGAGGTGACTCATTTACACCAATTTCCAAAGCTCAGATTGGTCTCCAG 472
QY 421 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 480
DB 473 AAGTACATTTAGAGCTGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 532
QY 481 ATAGTGTATTGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA 540
DB 533 ATAGTGTATTGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAAAA 592
QY 541 ACTCTTCAGGTGTAGAGAAAGGATTGAAATATTTATTCAGACATAAAATTTATAAAC 600
DB 593 ACTCTTCAGGTGTAGAGAAAGGATTGAAATATTTATTCAGACATAAAATTTATAAAC 652
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DB 653 TCTCACCAGAGACTACTTATTGCTTAAAGTTAAAGCAGCACTACTTACGTCTATGGAATA 712
QY 661 TTGGTGTCTATAGTCCAGTACATTTGATTAAGCCACAGTTGAAATGAACCTACCTCCAC 720
DB 713 TTGGTGTCTATAGTCCAGTACATTTGATTAAGCCACAGTTGAAATGAACCTACCTCCAC 772
QY 721 CAGAAAAATATAGAAAGTCTAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 780
DB 773 CAGAAAAATATAGAAAGTCTAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTTATACAT 832
QY 781 ATGCAAAACATGACCTTTCAAGTTCAAGTGGGTCTCAGCGCTTTTAAAAAGGAATCTCGGAA 840
DB 833 ATGCAAAACATGACCTTTCAAGTTCAAGTGGGTCTCAGCGCTTTTAAAAAGGAATCTCGGAA 892
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QY 841 ACCATTTGTATAAATGGAACCAATACCTGACTGTGAAATGTCAAAACTTACCAGTGTG 900
DB 893 ACCATTTGTATAAATGGAACCAATACCTGACTGTGAAATGTCAAAACTTACCAGTGTG 952
QY 901 TCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960
DB 953 TCTTTCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 1012
QY 961 GAAATAACACATCTTTTCTGCTGGAAGATGAAAGTTTGATCTGAAATACAAGCTTTCC 1020
DB 1013 GAAATAACACATCTTTTCTGCTGGAAGATGAAAGTTTGATCTGAAATACAAGCTTTCC 1072
QY 1021 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1080
DB 1073 TACTTCTCCAGTCTTTTAAACATTTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1132
QY 1081 CTCAAAAACAGTCTGAAAAACAGCCCTGTGATCCAGGATTTACCTGATTTTATGAATTA 1140
DB 1133 CTCAAAAACAGTCTGAAAAACAGCCCTGTGATCCAGGATTTATCCACTGATTTTATGAATTA 1192
QY 1141 TTTTGTGGGAAACACCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200
DB 1193 TTTTGTGGGAAACACCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1252
QY 1201 CAGTTCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACCATGG 1260
DB 1253 CAGTTCTTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGACACACCATGG 1312
QY 1261 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1320
DB 1313 ATGAAAGCTGAATAAAGCAGTGTGTTTGTAGTGACGCTGTATGTGAGAAAAACAAACCCAG 1372
QY 1321 GAAATACCTCTAAA 1334
DB 1373 GAAATACCTCTAAA 1386
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RESULT 12

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US-09-949-016-2769
; Sequence 2769, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2769
; LENGTH: 2753
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2769
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Query Match      98.7%; Score 1326; DB 3; Length 2753;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTCAGGGATCTGGCGGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 60
DB 53 CTGGTGGGATCTGGCGGGCTCCAGATGATGGTCTCTGGGCGGACGACCCCTAG 112
QY 61 TGCTCTGGCGGGTGGGCGGATGGTGTGTCGGAGCGGAGGTGGAAAAATCTAAAT 120
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Db 113 TGCTCGTGGCGTGGCCCATGGGTGTTGTCCGACGCGCGAGGTGGAAAAATCTAAAT 172  
Qy 121 CTCCTCAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTCGAGTGGGAACAGGA 180  
Db 173 CTCCTCAAAAGTAGAGGTGACATCATAGATGACAACTTTATCTCGAGTGGGAACAGGA 232  
Qy 181 GCGATGAGTCTGCGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 240  
Db 233 GCGATGAGTCTGCGGAATGTGACTTTTTCATTCGATTATCAAAAACTGGGATGGATA 292  
Qy 241 ATTGGATAAAATCTCTGGGGTGCAGATAATTTACTAGTACCAATGCAACTTTTCTTCAC 300  
Db 293 ATTGGATAAAATCTCTGGGGTGCAGATAATTTACTAGTACCAATGCAACTTTTCTTCAC 352  
Qy 301 TCAAGCTGAATGTTTATCAAGAAATTAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 360  
Db 353 TCAAGCTGAATGTTTATCAAGAAATTAATTTGCGTATAAGAGCAGAAAAAGAAACACTT 412  
Qy 361 CTTCACTGATAGAGTTGACTCATTTACACCAATTTGCGAAAGCTCAGATTGGTCTCCAG 420  
Db 413 CTTCACTGATAGAGTTGACTCATTTACACCAATTTGCGAAAGCTCAGATTGGTCTCCAG 472  
Qy 421 AAGTACATTTAGAGCTGAGATAAGCAATAGTATACATCTCTCTGGAACAAAAAG 480  
Db 473 AAGTACATTTAGAGCTGAGATAAGCAATAGTATACATCTCTCTGGAACAAAAAG 532  
Qy 481 ATAGTGTATGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 540  
Db 533 ATAGTGTATGCGGCTTTGATGTTTAAAGCTTTACATATAGCTTACTTATCTGGAATA 592  
Qy 541 ACTCTTCAGGTGTAGAGAAAGGATGAAATATTTATTCAGACATATAAAATTTATAAAC 600  
Db 593 ACTCTTCAGGTGTAGAGAAAGGATGAAATATTTATTCAGACATATAAAATTTATAAAC 652  
Qy 601 TCTCACCAGACACTTATTTGCTTAAAGTTAAAGCAGCACTACTACGTCATCGGAAA 660  
Db 653 TCTCACCAGACACTTATTTGCTTAAAGTTAAAGCAGCACTACTACGTCATCGGAAA 712  
Qy 661 TTGTTGCTATAGTCCAGTACATTTGATTAAGACCAAGTTGAAATGAACTACTCTCCAC 720  
Db 713 TTGTTGCTATAGTCCAGTACATTTGATTAAGACCAAGTTGAAATGAACTACTCTCCAC 772  
Qy 721 CAGAAAAATAGAAAGTCAAGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 780  
Db 773 CAGAAAAATAGAAAGTCAAGTCCAAAATCAGAACTATGTTCTTAAATGGGATATACAT 832  
Qy 781 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGGCTTTTAAAAAGGAATCTCGAA 840  
Db 833 ATGCAACATGACCTTTCAAGTTCAGTGGCTCCAGGCTTTTAAAAAGGAATCTCGAA 892  
Qy 841 ACCATTTGTATATAGTGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 900  
Db 893 ACCATTTGTATATAGTGAACAAATACCTGACTGTGAAATGTCAAACTACCCAGTGTG 952  
Qy 901 TCTTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCGGCTCAAGCACTCGATG 960  
Db 953 TCTTTCTCAAAAGCTTTTCCAAAAGGAATTTACCTTCTCGGCTCAAGCACTCGATG 1012  
Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC 1020  
Db 1013 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATCTGAAATACAAGCTTTCC 1072  
Qy 1021 TACTTCTCCAGTCTTTAAACATAGATCCCTTAGTGATTTCATTCATATCTATCCGTG 1080  
Db 1073 TACTTCTCCAGTCTTTAAACATAGATCCCTTAGTGATTTCATTCATATCTATCCGTG 1132  
Qy 1081 CTCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCACTGATTATGAAATTA 1140  
Db 1133 CTCAAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCACTGATTATGAAATTA 1192  
Qy 1141 TTTTGTGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Db 1193 TTTTGTGGAAAAACACTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1252

Qy 1201 CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1260  
Db 1253 CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG 1312  
Qy 1261 ATGAAAAAGCTGAATAAAAGCAGTGTGTTTATAGTACGCTGTATGTGAGAAAAACAAACCCAG 1320  
Db 1313 ATGAAAAAGCTGAATAAAAGCAGTGTGTTTATAGTACGCTGTATGTGAGAAAAACAAACCCAG 1372  
Qy 1321 GAAATACCTCTAAA 1334  
Db 1373 GAAATACCTCTAAA 1386

## RESULT 13

US-09-056-461-21  
; Sequence 21, Application US/09056461  
; Patent No. 6713609  
; GENERAL INFORMATION:  
; APPLICANT: Chuntharapai, Anon  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Love, Richard B.  
; APPLICANT: Lu, Ji  
; APPLICANT: Stewart, Timothy A.  
; TITLE OF INVENTION: Type I Interferon Receptor Antibodies  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,461  
; FILING DATE: 07-Apr-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/058212  
; FILING DATE: 16  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1039P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6741 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
US-09-056-461-21

Query Match 98.2%; Score 1318.6; DB 3; Length 6741;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1321; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 CTGAGGAGATCTGGGGCGGCTCCAGATGATGGTCTCTCTGGGGCGGAGACCCCTAG 60  
Db 12 CTGTGGGATCTGGGGCGGCTCCAGATGATGGTCTCTCTGGGGCGGAGACCCCTAG 71  
Qy 61 TGCTCGTCCGCTGGGCCCATGGGTGTTGTCGACAGCCGAGGTGGAATAATCTAAAAT 120  
Db 72 TGCTCGTCCGCTGGGCCCATGGGTGTTGTCGACAGCCGAGGTGGAATAATCTAAAAT 131  
Qy 121 CTCCTCAAAAGTAGAGGTGACATCATAGATGACAACTTTTATCTGAGGTGGAAACAGGA 180

Db 132 CTCTCAAAAAGTAGAGTCCACATCATAGATGACAACTTTATCTCGAGGTGGAACAGGA 191  
Qy 181 GCGATGAGTCTGTGGGAAATGTCATTTTTCATTCGATTATCAAAAACCTGGGATGGATA 240  
Db 192 GCGATGAGTCTGTGGGAAATGTCATTTTTCATTCGATTATCAAAAACCTGGGATGGATA 251  
Qy 241 ATTGGATAAAATTTGTCTGGGTGTGAGAAATTAATTTGGGTATAAGAGCAGAAAAACCACTT 300  
Db 252 ATTGGATAAAATTTGTCTGGGTGTGAGAAATTAATTTGGGTATAAGAGCAGAAAAACCACTT 311  
Qy 301 TCAAGCTGAATGTTTATGAGAAATTAATTTGGGTATAAGAGCAGAAAAACCACTT 360  
Db 312 TCAAGCTGAATGTTTATGAGAAATTAATTTGGGTATAAGAGCAGAAAAACCACTT 371  
Qy 361 CTTTCATGATAGAGTGTGAGTCTTACACCAATTTGCGAAGCTCAGATTGCTCTCCAG 420  
Db 372 CTTTCATGATAGAGTGTGAGTCTTACACCAATTTGCGAAGCTCAGATTGCTCTCCAG 431  
Qy 421 AAGTACATTTAGAGCTGGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 480  
Db 432 AAGTACATTTAGAGCTGGAAGATAAGGCAATAGTGATACACATCTCTCTCGGAACAAAAG 491  
Qy 481 ATAGTGTTATGTGGGCTTTGGAGTTTAAAGCTTTACATATAGTTACTTATCTGGAAAA 540  
Db 492 ATAGTGTTATGTGGGCTTTGGAGTTTAAAGCTTTACATATAGTTACTTATCTGGAAAA 551  
Qy 541 ACTCTTCAGGTGTAGAGAAAGGTTGAAAATTTATTTCCAGACATATAAATTTATAAC 600  
Db 552 ACTCTTCAGGTGTAGAGAAAGGTTGAAAATTTATTTCCAGACATATAAATTTATAAC 611  
Qy 601 TCTCACCAGAGACTACTTATTTGCTAAAGTTAAAGCAGCACTACTTACGTCTCATGGAAAA 660  
Db 612 TCTCACCAGAGACTACTTATTTGCTAAAGTTAAAGCAGCACTACTTACGTCTCATGGAAAA 671  
Qy 661 TTGGTGTCTATAGTCCAGTACATTTGATTAAGAACCAAGTTGAAATGAACTACCTCCAC 720  
Db 672 TTGGTGTCTATAGTCCAGTACATTTGATTAAGAACCAAGTTGAAATGAACTACCTCCAC 731  
Qy 721 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTTAAATGGGATATACAT 780  
Db 732 CAGAAAATATAGAGTCAAGTGTCCAAATCAGAACTATGTTTAAATGGGATATACAT 791  
Qy 781 ATGCAAAACATGACCTTTCAAGTTCAAGTGTCCAGCGCTTTTAAAGAAAGAACTCTGGAA 840  
Db 792 ATGCAAAACATGACCTTTCAAGTTCAAGTGTCCAGCGCTTTTAAAGAAAGAACTCTGGAA 851  
Qy 841 ACCAATTTGATTAATGGAACAAATACCTGACTGTGAAATGTCAAAATACCCAGGTG 900  
Db 852 ACCAATTTGATTAATGGAACAAATACCTGACTGTGAAATGTCAAAATACCCAGGTG 911  
Qy 901 TCTTTCTCAAAAGCTTTTCCAAAAGAAATTTACCTTCTCCGGTCAAGCATCTGATG 960  
Db 912 TCTTTCTCAAAAGCTTTTCCAAAAGAAATTTACCTTCTCCGGTCAAGCATCTGATG 971  
Qy 961 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGTACTGAAATCAAGCTTTCC 1020  
Db 972 GAAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGTACTGAAATCAAGCTTTCC 1031  
Qy 1021 TACTTCTCCAGTCTTTAAACATTAAGTCCCTTGTAGTCAATTCATATATATCGGTG 1080  
Db 1032 TACTTCTCCAGTCTTTAAACATTAAGTCCCTTGTAGTCAATTCATATATATCGGTG 1091  
Qy 1081 CTCCAAAACAGTCTGGAAACACGCTGTGATCCAGGATTTATCCATGATTTATGAATTA 1140  
Db 1092 CTCCAAAACAGTCTGGAAACACGCTGTGATCCAGGATTTATCCATGATTTATGAATTA 1151  
Qy 1141 TTTTTCGGGAAAAACATTTCAATCTCAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1200  
Db 1152 TTTTTCGGGAAAAACATTTCAATCTCAGAGAAAAATTTATCGAGAAAAAACTGATGTTA 1211  
Qy 1201 CAGTTCCTAATTTGAAACCACTGACTGTATATTTGTGAAAGCCAGAGCAACACCATGG 1260

Db 1212 CAGTTCCTAATTTGAAACCACTGACTGTATATTTGTGTGAAAGCCAGAGCACACACCATGG 1271  
Qy 1261 ATGAAAGCTGAATAAAGCAGGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAACACAG 1320  
Db 1272 ATGAAAGCTGAATAAAGCAGGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAACACAG 1331  
Qy 1321 GAAAT 1325  
Db 1332 GAAAT 1336

RESULT 14  
US-09-949-016-11843  
; Sequence 11843, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11843  
; LENGTH: 35574  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-11843

Query Match 18.7%; Score 251.8; DB 3; Length 35574;  
Best Local Similarity 76.9%; Pred. No. 9.2e-60;  
Matches 367; Conservative 0; Mismatches 12; Indels 98; Gaps 1;

Qy 815 CGCTTTTAAAGAAATCCTGGAAACCAATTTGTATAATGGAAACAAATACCTGACTG 874  
Db 26115 CGCTTTTAAAGAAATCCTGGAAACCAATTTGTATAATGGAAACAAATACCTGACTG 26174  
Qy 875 TGAABATGTCAAACTACCCAGTGTCTTCTCAAAAGCTTTTCCAAAAGGAATTTA 934  
Db 26175 TGAABATGTCAAACTACCCAGTGTCTTCTCAAAAGCTTTTCCAAAAGGAATTTA 26234  
Qy 935 CTTTCTCCGCTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGGAAGATATA 994  
Db 26235 CTTTCTCCGCTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGGAAGATATA 26294  
Qy 995 GTTGTACTGAAATACA----- 1012  
Db 26295 GTTGTACTGAAATACAAGTAAGGACGAGTAGTTTTTACTGGAGATTGTAATTTCTCTGGT 26354  
Qy 1013 -----AGCT 1016  
Db 26355 GCAAGTTTTAAATTTGTTTTCTAAATGAAACATTAATTTCTTACAAATTTTTCTAGCT 26414  
Qy 1017 TTCTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCAATTCATATATATC 1076  
Db 26415 TTCTACTTCTCCAGTCTTTAAACATTAGATCCCTTAGTGATTCAATTCATATATATC 26474  
Qy 1077 GGTGCTCCAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCAGTATTATGAA 1136  
Db 26475 GGTGCTCCAAAACAGTCTGGAACACGCTGTGATCCAGGATTTATCCAGTATTATGAA 26534  
Qy 1137 ATTATTTTGGGAAAAACCTTCAAAATGCTGAGAGAAAAATTTATCGAGAAAAAACT 1193  
Db 26535 ATTATTTTGGGAAAAACCTTCAAAATGCTGAGGTAAGAAAGACTGTATAGTATAAT 26591

## RESULT 15

US-09-949-016-14511  
; Sequence 14511, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C0001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14511  
; LENGTH: 35574  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14511

Query Match 18.7%; Score 251.8; DB 3; Length 35574;

Best Local Similarity 76.9%; Pred. No. 9.2e-60;

Matches 367; Conservative 0; Mismatches 12; Indels 98; Gaps 1;

Qy	815	CGCCTTTTAAAGGAATCTCGAAACCATTTCTGTATAATGGAACAAATACCTGACTG	874
Db	26115	CGCCTTTTAAAGGAATCTCGAAACCATTTCTGTATAATGGAACAAATACCTGACTG	26174
Qy	875	TGAAATGTCAAACTACCCAGTGTCTTTCTCAAAACGTTTTCCAAAAGGAATTTA	934
Db	26175	TGAAATGTCAAACTACCCAGTGTCTTTCTCAAAACGTTTTCCAAAAGGAATTTA	26234
Qy	935	CTTCTCCGGGTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGAAGAGATAA	994
Db	26235	CTTCTCCGGGTACAAGCATCTGATGGAATAACACATCTTTTGGTCTGAAGAGATAA	26294
Qy	995	GTTTGATCTGAATACA-----	1012
Db	26295	GTTTGATCTGAATACAAGGTAAAGGCAGTAGTTTCTGAGAGATTGTAATCTCTGGT	26354
Qy	1013	-----AGCT	1016
Db	26355	GCAAGTTTTTAAATTTGTTTCTTAATTGAACATATTTCTTTACAAATTTTCTAGCT	26414
Qy	1017	TTCTACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGATTCATTCATATATATC	1076
Db	26415	TTCTACTTCTCCAGTCTTTTAAACATTAGATCCCTTAGTGATTCATTCATATATATC	26474
Qy	1077	GGTGCTCCAAACAGCTCTGGAAACACGCTGTGATCCAGGATTATCCACTGATTATGAA	1136
Db	26475	GGTGCTCCAAACAGCTCTGGAAACACGCTGTGATCCAGGATTATCCACTGATTATGAA	26534
Qy	1137	ATTATTTTTTGGGAAACACCTTCAATGCTCAGAGAGAAAATTTATCGAGAAAAAACT	1193
Db	26535	ATTATTTTTTGGGAAACACCTTCAATGCTCAGAGAGAAAATTTATCGAGAAAATTT	26591

Search completed: January 17, 2006, 23:26:06

Job time : 270 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:10:37 ; Search time 32.8172 Seconds  
(without alignments)  
1098.405 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVLLGATTLVAVGPWV.....KSSVFSDAVCEKTPGNTSK 436

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgm2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgm2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SUMMARIES				ID	Description
	Score	Query Match	Length	DB		
1	2313	100.0	436	1	US-08-307-588-2	Sequence 2, Appli
2	2313	100.0	436	2	US-07-971-834-2	Sequence 2, Appli
3	2313	100.0	436	2	US-09-240-675-2	Sequence 2, Appli
4	2313	100.0	557	1	US-08-328-256-10	Sequence 10, Appli
5	2313	100.0	557	1	US-08-471-454-2	Sequence 2, Appli
6	2313	100.0	557	1	US-08-466-974-2	Sequence 2, Appli
7	2313	100.0	557	1	US-08-471-453-2	Sequence 2, Appli
8	2313	100.0	557	1	US-08-307-588-4	Sequence 4, Appli
9	2313	100.0	557	2	US-07-971-834-4	Sequence 4, Appli
10	2313	100.0	557	2	US-09-240-675-4	Sequence 4, Appli
11	2313	100.0	557	2	US-09-949-016-5972	Sequence 5972, Ap
12	2304	99.6	575	2	US-09-949-016-8640	Sequence 8640, Ap
13	2265	97.9	434	1	US-08-328-256-11	Sequence 11, Appli
14	2213	95.7	496	1	US-08-328-256-12	Sequence 12, Appli
15	2158	93.3	631	2	US-09-056-461-22	Sequence 22, Appli
16	1172	50.7	224	2	US-08-871-572B-9	Sequence 9, Appli
17	1141	49.3	226	2	US-08-871-572B-10	Sequence 10, Appli
18	781.5	33.8	224	2	US-08-871-572B-13	Sequence 13, Appli
19	720.5	31.2	227	2	US-08-871-572B-14	Sequence 14, Appli
20	588.5	25.4	224	2	US-08-871-572B-11	Sequence 11, Appli
21	490.5	21.2	202	4	PCT-US94-14277-3	Sequence 3, Appli
22	480.5	20.8	219	2	US-08-871-572B-12	Sequence 12, Appli
23	466.5	20.2	200	4	PCT-US94-14277-4	Sequence 4, Appli
24	228.5	9.9	233	2	US-08-871-572B-8	Sequence 8, Appli
25	228.5	9.9	273	2	US-09-949-016-11056	Sequence 11056, A
26	228.5	9.9	325	1	US-08-683-743-4	Sequence 4, Appli
27	228.5	9.9	325	2	US-09-870-574-3	Sequence 3, Appli

Query Match 100.0% Score 2313; DB 1; Length 436;

28	228.5	9.9	325	2	US-09-265-540E-6	Sequence 6, Appli
29	214	9.3	199	2	US-10-090-365-35	Sequence 35, Appli
30	214	9.3	199	2	US-09-728-911-35	Sequence 35, Appli
31	203	8.8	332	4	PCT-US94-14277-2	Sequence 2, Appli
32	200	8.6	567	2	US-09-949-016-11502	Sequence 11502, A
33	198	8.6	553	1	US-08-943-087-2	Sequence 2, Appli
34	198	8.6	553	1	US-08-943-087-14	Sequence 14, Appli
35	198	8.6	553	1	US-08-943-087-16	Sequence 16, Appli
36	198	8.6	553	1	US-08-943-087-18	Sequence 18, Appli
37	198	8.6	553	1	US-08-943-087-20	Sequence 20, Appli
38	198	8.6	553	1	US-08-943-087-22	Sequence 22, Appli
39	198	8.6	553	1	US-08-943-087-24	Sequence 24, Appli
40	198	8.6	553	1	US-08-943-087-26	Sequence 26, Appli
41	198	8.6	553	1	US-08-943-087-28	Sequence 28, Appli
42	198	8.6	553	1	US-08-943-087-30	Sequence 30, Appli
43	198	8.6	553	1	US-08-943-087-32	Sequence 32, Appli
44	198	8.6	553	1	US-08-943-087-34	Sequence 34, Appli
45	198	8.6	553	1	US-08-943-087-36	Sequence 36, Appli

ALIGNMENTS

RESULT 1  
US-08-307-588-2  
; Sequence 2, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: FLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 436 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-307-588-2

```
Best Local Similarity 100.0%; Pred. No. 9.2e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESVCNVT 60
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESVCNVT 60
Qy 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKNVYEEIKLIRAEKENTSSWYEVDSF 120
Db 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKNVYEEIKLIRAEKENTSSWYEVDSF 120
Qy 121 TPRKQAGIPPEVHLEAEKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180
Db 121 TPRKQAGIPPEVHLEAEKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180
Qy 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Db 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Qy 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
Qy 301 GIYLLRQVQSDGNNTSFWSEIEKFDTEIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GIYLLRQVQSDGNNTSFWSEIEKFDTEIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Qy 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 2
US-07-971-834-2
; Sequence 2, Application US/07971834
; Patent No. 6475983
; GENERAL INFORMATION:
; APPLICANT: EID, Pierre
; APPLICANT: GRESSER, Ion
; APPLICANT: LUTFALLA, Georges
; APPLICANT: MEYER, Francois
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: TOVEY, Michael
; APPLICANT: UZE, Gilles
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH
; AFFINITY FOR INTERFERONS ALPHA AND BETA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/07/971,834
; APPLICATION NUMBER: 17-FEB-1993
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR91/00318
; FILING DATE: 17-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
```

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; REFERENCE/DOCKET NUMBER: EID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-971-834-2

Query Match 100.0%; Score 2313; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 9.2e-230;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESVCNVT 60
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESVCNVT 60
Qy 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKNVYEEIKLIRAEKENTSSWYEVDSF 120
Db 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSLLKNVYEEIKLIRAEKENTSSWYEVDSF 120
Qy 121 TPRKQAGIPPEVHLEAEKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180
Db 121 TPRKQAGIPPEVHLEAEKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180
Qy 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Db 181 ENIYSRHKIYKLPSETTYCLKVAALLTSWKIGVSPVHCITKTVENELPPPENIEVSQ 240
Qy 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
Qy 301 GIYLLRQVQSDGNNTSFWSEIEKFDTEIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Db 301 GIYLLRQVQSDGNNTSFWSEIEKFDTEIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTP 360
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
Qy 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 3
US-09-240-675-2
; Sequence 2, Application US/09240675
; Patent No. 6787634
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; TITLE OF INVENTION: INTERFERON
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,675  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/307,588  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 436 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-240-675-2

Query Match 100.0%; Score 2313; DB 2; Length 436;  
Best Local Similarity 100.0%; Pred. No. 9,2e-230;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGNLSPKQVEVDIIDDNFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLSPKQVEVDIIDDNFILRNRSDESQVNT 60

Qy 61 FSPDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEDSF 120

Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180

Qy 181 ENIYSRHKIYKLPSTTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLPSTTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240

Qy 241 NONVYLKWDYTYANMTFOVWLHAFLENPGNHLKWKQIIPDCENVKTTQCVFQNVFQK 300  
Db 241 NONVYLKWDYTYANMTFOVWLHAFLENPGNHLKWKQIIPDCENVKTTQCVFQNVFQK 300

Qy 301 GIYLLRQVQSGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIAPKQSGNTP 360  
Db 301 GIYLLRQVQSGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIAPKQSGNTP 360

Qy 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 4

US-08-328-256-10  
Sequence 10, Application US/08328256  
Patent No. 5643749  
GENERAL INFORMATION:  
APPLICANT: REVEL, Michel  
APPLICANT: ABRAMOVICH, Carolina  
APPLICANT: RATOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERPERON ALPHA-RECEPTOR, ITS  
TITLE OF INVENTION: PREPARATION AND USE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/328,256  
FILING DATE: 24-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107378  
FILING DATE: 24-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: REVEL=13  
REFERENCE/DOCKET NUMBER: 25,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-328-256-10

Query Match 100.0%; Score 2313; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGNLSPKQVEVDIIDDNFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLSPKQVEVDIIDDNFILRNRSDESQVNT 60

Qy 61 FSPDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEDSF 120

Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180

Qy 181 ENIYSRHKIYKLPSTTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLPSTTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240

Qy 241 NONVYLKWDYTYANMTFOVWLHAFLENPGNHLKWKQIIPDCENVKTTQCVFQNVFQK 300  
Db 241 NONVYLKWDYTYANMTFOVWLHAFLENPGNHLKWKQIIPDCENVKTTQCVFQNVFQK 300

Qy 301 GIYLLRQVQSGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIAPKQSGNTP 360  
Db 301 GIYLLRQVQSGNNTSPWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIAPKQSGNTP 360

Qy 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

```

RESULT 5
US-08-471-454-2
; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-454-2

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-229;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPNVLSAAGGKNLKSQKVEVDIIDDNFILRNRSDESQVNT 60
Db 1 MMVLLGATTLVLVAVGPNVLSAAGGKNLKSQKVEVDIIDDNFILRNRSDESQVNT 60
Qy 61 FSPDYQKTGMNDWIKLSGQNITKCNFSLKLNVEEIKLRIRAEKNTSSWYVDSP 120
Db 61 FSPDYQKTGMNDWIKLSGQNITKCNFSLKLNVEEIKLRIRAEKNTSSWYVDSP 120
Qy 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSGVBEI 180
Db 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSGVBEI 180
Qy 181 ENIYSRHKIYKLSPTTYCLVKKALITSNKIGVYSPVHCIKTTVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPTTYCLVKKALITSNKIGVYSPVHCIKTTVENELPPENIEVSQ 240

RESULT 6
US-08-466-974-2
; Sequence 2, Application US/08466974
; Patent No. 5861258
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,974
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-974-2

Query Match 100.0%; Score 2313; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.4e-229;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPNVLSAAGGKNLKSQKVEVDIIDDNFILRNRSDESQVNT 60
Db 1 MMVLLGATTLVLVAVGPNVLSAAGGKNLKSQKVEVDIIDDNFILRNRSDESQVNT 60
Qy 61 FSPDYQKTGMNDWIKLSGQNITKCNFSLKLNVEEIKLRIRAEKNTSSWYVDSP 120
Db 61 FSPDYQKTGMNDWIKLSGQNITKCNFSLKLNVEEIKLRIRAEKNTSSWYVDSP 120
Qy 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSGVBEI 180
Db 121 TPRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSGVBEI 180
Qy 181 ENIYSRHKIYKLSPTTYCLVKKALITSNKIGVYSPVHCIKTTVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPTTYCLVKKALITSNKIGVYSPVHCIKTTVENELPPENIEVSQ 240
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Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLSPKQVEVDIIDDNFILRWNRSDESNGVT 60  
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Db 61 FSDYQKTGMDNWKLSGCONITSTKCNFSLKLVNVEEIKLIRAEKENTSSWYEDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFYSLIWKNSGVEERI 180  
Qy 181 ENIYSRHKIKYKSPETTYCLVKVKAALITSWKIGYVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIKYKSPETTYCLVKVKAALITSWKIGYVSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NQNTVLKWDITYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTCQVFPQNVFQK 300  
Db 241 NQNTVLKWDITYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTCQVFPQNVFQK 300  
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Db 301 GIVLLRVOASDGNNTSPWSEBEIKPDTETIQAPLLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNARERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 7

US-08-471-453-2  
; Sequence 2, Application US/08471453  
; Patent No. 5886153  
; GENERAL INFORMATION:  
; APPLICANT: MOGENSEN, Knud E.  
; APPLICANT: UZE, Gilles  
; APPLICANT: LUTFALLA, Georges  
; APPLICANT: GRESSER, Ion  
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,453  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/900,642  
; FILING DATE: 15-JUN-1992  
; APPLICATION NUMBER: FR 89/13770  
; FILING DATE: 20-OCT-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BYRNE, THOMAS E.  
; REGISTRATION NUMBER: 32,205  
; REFERENCE/DOCKET NUMBER: 960-7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-453-2

Query Match 100.0%; Score 2313; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLSPKQVEVDIIDDNFILRWNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLSPKQVEVDIIDDNFILRWNRSDESNGVT 60  
Qy 61 FSDYQKTGMDNWKLSGCONITSTKCNFSLKLVNVEEIKLIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMDNWKLSGCONITSTKCNFSLKLVNVEEIKLIRAEKENTSSWYEDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFYSLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFYSLIWKNSGVEERI 180  
Qy 181 ENIYSRHKIKYKSPETTYCLVKVKAALITSWKIGYVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIKYKSPETTYCLVKVKAALITSWKIGYVSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NQNTVLKWDITYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTCQVFPQNVFQK 300  
Db 241 NQNTVLKWDITYANMTFQVQWLHAFKRNPGNHLKWKQIPDCENVKTTCQVFPQNVFQK 300  
Qy 301 GIVLLRVOASDGNNTSPWSEBEIKPDTETIQAPLLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360  
Db 301 GIVLLRVOASDGNNTSPWSEBEIKPDTETIQAPLLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNARERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 8

US-08-307-588-4  
; Sequence 4, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588  
FILING DATE: 05-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-307-588-4

Query Match 100.0%; Score 2313; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESIGNVT 60  
DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESIGNVT 60  
QY 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
DB 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
QY 241 QNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 QNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSEEEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSEEEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

## RESULT 9

US-07-971-834-4  
Sequence 4, Application US/07971834  
Patent No. 6475983  
GENERAL INFORMATION:  
APPLICANT: Eid, Pierre  
APPLICANT: GRESSER, Ion  
APPLICANT: LUTFALLA, Georges  
APPLICANT: MEYER, Francois  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: TOVEY, Michael  
APPLICANT: UZE, Gilles  
TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH

TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,834  
FILING DATE: 17-FEB-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR91/00318  
FILING DATE: 17-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: EID=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-971-834-4

Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESIGNVT 60  
DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESIGNVT 60  
QY 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
DB 61 FSPDYQKTGMNDWIKLSGCCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
DB 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
QY 241 QNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 QNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSEEEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSEEEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 10  
US-09-240-675-4  
; Sequence 4, Application US/09240675  
; Patent No. 6787634  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,675  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-240-675-4

Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESQVNT 60  
Qy 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVBERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVBERI 180  
Qy 181 ENISVRHKIYKLSPTTYCLVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENISVRHKIYKLSPTTYCLVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300

Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300  
Qy 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Qy 361 VIQDYPLIYIIFWENTSNAERKIIIEKTDVTVNPKPLTVYCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYIIFWENTSNAERKIIIEKTDVTVNPKPLTVYCVKARAHMTWDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436  
RESULT 11  
US-09-949-016-5972  
; Sequence 5972, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5972  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-5972

Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1.4e-229;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVAVGFWLVAAGGKLNKSPQKVEVDIIDDNFILRNRSDESQVNT 60  
Qy 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSCQNTSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVBERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNSSGVBERI 180  
Qy 181 ENISVRHKIYKLSPTTYCLVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENISVRHKIYKLSPTTYCLVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300  
Qy 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Qy 361 VIQDYPLIYIIFWENTSNAERKIIIEKTDVTVNPKPLTVYCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYIIFWENTSNAERKIIIEKTDVTVNPKPLTVYCVKARAHMTWDEKLNKSSV 420

Qy 421 FSDAVCEKTPGNTSK 436  
Db 421 FSDAVCEKTPGNTSK 436

## RESULT 12

US-09-949-016-8640  
; Sequence 8640, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8640  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8640

Query Match 99.6%; Score 2304; DB 2; Length 575;  
Best Local Similarity 99.5%; Pred. No. 1.2e-228;  
Matches 434; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGKNLKSQKVEVDIIDNFIILNRNRSDESGVNT 60  
Db 19 MMVLLGATTLVLVAVAPWLSAAAGKNLKSQKVEVDIIDNFIILNRNRSDESGVNT 78  
Qy 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 120  
Db 79 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 138  
Qy 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Db 139 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 198  
Qy 181 ENIYSRHKIYKLSPETTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 199 ENIYSRHKIYKLSPETTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 258  
Qy 241 NQNVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Db 259 NQNVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 318  
Qy 301 GIYLLRVQASDGNNTSFWSSEIKFDETEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
Db 319 GIYLLRVQASDGNNTSFWSSEIKFDETEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 378  
Qy 361 VIQDYPLIYIIFWNTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSSV 420  
Db 379 VIQDYPLIYIIFWNTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSSV 438  
Qy 421 FSDAVCEKTPGNTSK 436  
Db 439 FSDAVCEKTPGNTSK 454

## RESULT 13

US-08-328-256-11  
; Sequence 11, Application US/08328256  
; Patent No. 5643749  
; GENERAL INFORMATION:  
; APPLICANT: REVEL, Michel

; APPLICANT: ABRAMOVICH, Carolina  
; APPLICANT: RATOVITSKI, Edward  
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,256  
; FILING DATE: 24-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107378  
; FILING DATE: 24-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: REVEL=13  
; REFERENCE/DOCKET NUMBER: 25,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 434 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-328-256-11

Query Match 97.9%; Score 2265; DB 1; Length 434;  
Best Local Similarity 100.0%; Pred. No. 8.2e-225;  
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGKNLKSQKVEVDIIDNFIILNRNRSDESGVNT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGKNLKSQKVEVDIIDNFIILNRNRSDESGVNT 60  
Qy 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPETTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NQNVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NQNVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRVQASDGNNTSFWSSEIKFDETEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSSEIKFDETEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYIIFWNTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSSV 420  
Db 361 VIQDYPLIYIIFWNTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSSV 420  
Qy 421 FSDAVCE 427

```
Db      421 FSDAVE 427
|||||
RESULT 14
US-08-328-256-12
; Sequence 12, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL=13
; REFERENCE/DOCKET NUMBER: 25,618
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-12

Query Match      95.7%; Score 2213; DB 1; Length 496;
Best Local Similarity 98.1%; Pred. No. 2,4e-219;
Matches 419; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

Qy      1  MVVLLGATTLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNRSDESVCVNT 60
Db      1  MVVLLGATTLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNRSDESVCVNT 60

Qy      61  FSPDYQKTMNDWIKLSGCONITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDVSF 120
Db      61  FSPDYQKTMNDWIKLSGCONITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDVSF 120

Qy      121  TPFRKAQIGPPPVHLEAEDKATVIHISPTGKDSVNMWALDGLSFTYSLLIWKNSSGVBERI 180
Db      121  TPFRKAQIGPPPVHLEAEDKALVIHISPTGKDSVNMWALDGLSFTYSLLIWKNSSGVBERI 180

Qy      181  ENIYSRHKIYKLSPEYTYCLVKAALLTSWKIGVYSPVHCIKTTVENELPPPEVSVQ 240
Db      181  ENIYSRHKIYKLSPEYTYCLVKAALLTSWKIGVYSPVHCIKTTVENELPPPEVSVQ 240

Qy      241  NONVYLKWDYTYANNMTFQVQMLHAFKRNPGNHLKYKQIPDCENVTTCQVFPQNFQK 300
Db      241  NONVYLKWDYTYANNMTFQVQMLHAFKRNPGNHLKYKQIPDCENVTTCQVFPQNFQK 300

Qy      301  GIYLLRVQASDGNNTSFWSSEIKEDTEIQAPLLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360
Db      301  GIYLLRVQASDGNNTSFWSSEIKEDTEIQAPLLPPVFNIRSLSDSFHYIIGAPKQSGNTP 360

Qy      361  VIQDYPLIYELIFWENTSNARKEIIKKTDVTVNPKPLTVYCVKARAHWTWDEKLNKSSV 420
Db      361  VIQDYPLIYELIFWENTSNARKEIIKKTDVTVNPKPLTVYCVKARAHWTWDE----- 413

Qy      421  FSDAVE 427
Db      414  -SDAVE 419

RESULT 15
US-09-056-461-22
; Sequence 22, Application US/09056461
; Patent No. 6713609
; GENERAL INFORMATION:
; APPLICANT: Chunharapai, Anon
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Love, Richard B.
; APPLICANT: Lu, Ji
; APPLICANT: Stewart, Timothy A.
; TITLE OF INVENTION: Type I Interferon Receptor Antibodies
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,461
; FILING DATE: 07-Apr-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/058212
; FILING DATE: 16
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1039P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-461-22

Query Match      93.3%; Score 2158; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.7e-213;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      30  LKSPQKVEVDIIDNFIILNRNRSDESVCVNTFSFDYQKTMNDWIKLSGCONITSTKCNF 89
Db      1  LKSPQKVEVDIIDNFIILNRNRSDESVCVNTFSFDYQKTMNDWIKLSGCONITSTKCNF 60

Qy      90  SSLKLVYEEIKLIRAEKENTSSWYEDVSTTPFRKAQIGPPEVHLEAEDKALVIHISPG 149
Db      61  SSLKLVYEEIKLIRAEKENTSSWYEDVSTTPFRKAQIGPPEVHLEAEDKALVIHISPG 120

Qy      150  TKDSVNMWALDGLSFTYSLLIWKNSSGVBERIENTYSRHKIYKLSPEYTYCLVKAALLTS 209
Db      150  TKDSVNMWALDGLSFTYSLLIWKNSSGVBERIENTYSRHKIYKLSPEYTYCLVKAALLTS 209
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Db	121	TKDSVMWALDGLSFTYSLLIWKNSGVEERIENTYSRHKIYKLSPETTYCLKVKAALLTS	180
Qy	210	WKIGVISPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAFLEKRN	269
Db	181	WKIGVISPVHCICKTTVENELPPPENIEVSQONQYVLKWDYTYANMTFQVQWLHAFLEKRN	240
Qy	270	PGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQ	329
Db	241	PGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQ	300
Qy	330	AFLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIODYPLIYEIIFWENTNAERKIIIEKKT	389
Db	301	AFLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIODYPLIYEIIFWENTNAERKIIIEKKT	360
Qy	390	DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGN	433
Db	361	DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGN	404

Search completed: January 17, 2006, 07:20:56  
Job time : 33.8172 secs











[illegible]

Qy 231 PPEINIEVSQNQNVYVLKWD-----YYANMTFQVOWLHAFLEKRP-GNHLYKWK 278  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
610 PSRNTDTSV-----VSWSEESKDAKELVGYIEANVAGSGKWEFC--NNNPVKTHRF--- 659  
Qy 279 QIPDCENNVKTQCVPFNQVFKGIYLRLVQASDGNNSTFWSEEIKPTEIOAFLLP--- 335  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
660 ---TCHGLVTCQS-----YIFRVAVNAAGLSEYSQDSE-AIEVKAIAPPSP 704  
Qy 336 --VFNIIRLSDSFHIIYGAPKQSGNTPVIODIPLIYEII-----FMWENTSNAERKIIEKK 388  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
705 CDITCLESFRSDSMVLGKWKQPKDTGAEITGVYNYREVIDGVPCWR---EAVNKAVREE 761  
Qy 389 TDVTVPNLKELTYCVKARAHHTMDEKLKNSVFSDAVCEK 428  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
762 A-YKISLNKENMVYFOVAAMNMAGLGAPSAVSECPCKEE 800

RESULT 12  
F90109  
Splicing factor Prp8 [imported] - Guillardia theta nucleomorph  
C;Species: nucleomorph Guillardia theta  
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: F90109  
C;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif  
Nature 410, 1091-1096, 2001  
A;Title: The highly reduced genome of an enslaved algal nucleus.  
A;Reference number: A99082; MUID:11323671; PMID:11323671  
A;Accession: F90109  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-2057 <DOU>  
A;Cross-references: UNIPROT:Q9AW36; UNIPARC:UPI00000A2A43; GB:AJO10592; NID:g12580717; E  
C;Genetics:  
A;Map position: 2  
A;Genome: nucleomorph  
C;Keywords: nucleomorph

Query Match 5.2%; Score 120; DB 2; Length 2057;  
Best Local Similarity 18.8%; Pred.No.2.1;  
Matches 95; Conservative 80; Mismatches 151; Indels 180; Gaps 24;

Qy 43 DNFILNRNRSDESNGVTFSDYQTKGMWNKILSGCONITSTKCNPSLLKNVYBEIKL 102  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
913 NNFIQL-----FYFIVDISLGIKNIIYV-----ISSKKTENSFPFEIKSKEKII 958  
Qy 103 RIR-----AEKNTSGSWEZ-----DSFTPFKAOIGPVEHVLEADKAIVIHIS 147  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
959 YMYRIEQIYIQIKEGNKTIIDYMDHLKKNFRAKLEKSILKPNLFNLFKLEISICRHVL 1018  
Qy 148 PGTKDSVMWALDGLSFYSLIWNKSSGVEERIEN--IYSRHKIYKLSPTTYCLAKVAA 205  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
1019 DRRNDLT-----IGFSQMLLYSYESTLTKVKKNFPIFNNFKICNISIK-LFOLQKNKF 1072  
Qy 206 LLTS-----WKIGVYSPVHC-----IKTTVENE 228  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
1073 LLTSGSSSPSKLIKWN-GILLGYCFEFRKALVSSQNFTTRLKYEKEIIANKASLSK 1131  
Qy 229 LPP-----PEN-----IEVSQNQNVYVLKWDYTYANMTF 257  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
1132 MPSRFPVLPFPKPKEFGGLGMLSIFYNYIPENDLKSCLKMWISKNSNL---NYTNLSITKF 1188  
Qy 258 QVOWLHAFLRNPGNHLYKWQIPDC-ENVKTTQC-VFPQ---NVFOKGI----- 302  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
1189 IKDWTNEFKSN-----IAWKGLILKKNFKGRIKIYQKISNFLKGKGPRIETIFSXY 1243  
Qy 303 -----YLLRVQASDGNNSTFWSEBEIKPTEIOAFLLPVFNIRLSLD 344  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :  
1244 RLFLPYDYGWRLNLDLSRYIL-----STWNSFWTWTSKPHEGKL-----YNLSYNN 1289  
Qy 345 SFHIYIGAPKQSGNTPVIODIPLI-----YEIFEWENTSNAERKIIEKKTDTVTPNLK 397  
Db : | : | : | : | : | : | : | : | : | : | : | : | : | :

[illegible]



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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 07:18:53 ; Search time 88.5544 Seconds  
(without alignments)  
2057.195 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVLLGATTLVLVAGPWV.....KSSVFSDAVCKTKRGNTSK 436

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2313	100.0	436	3	US-09-240-675-2
2	2313	100.0	436	4	US-10-824-981-2
3	2313	100.0	436	5	US-10-473-127-1756
4	2313	100.0	436	5	US-10-473-127-1758
5	2313	100.0	436	5	US-10-473-127-1764
6	2313	100.0	557	3	US-09-240-675-4
7	2313	100.0	557	4	US-10-358-228-3
8	2313	100.0	557	5	US-10-473-127-1757
9	2313	100.0	557	5	US-10-473-127-1759
10	2313	100.0	557	5	US-10-473-127-1760
11	2313	100.0	557	5	US-10-473-127-1763
12	2313	100.0	557	5	US-10-473-127-1765
13	2313	100.0	557	5	US-10-473-127-1766
14	2313	100.0	557	5	US-10-473-127-1772
15	2313	100.0	557	5	US-10-473-127-1773
16	2309	99.8	557	5	US-10-473-127-1768
17	2308	99.8	557	4	US-10-824-981-4
18	2308	99.8	557	5	US-10-473-127-1769
19	2307	99.7	557	5	US-10-473-127-1761
20	2304	99.6	436	5	US-10-473-127-1767
21	2302	99.5	575	3	US-09-925-300-1672
22	2302	99.5	575	5	US-10-473-127-1762
23	2287	98.9	575	5	US-10-450-763-47653
24	2279	98.5	441	5	US-10-764-833-41
25	2260	97.7	434	5	US-10-473-127-1770
26	2208	95.5	496	5	US-10-473-127-1771
27	1507	65.2	560	4	US-10-293-832-29

28 1500 64.9 560 4 US-10-293-832-30 Sequence 30, Appl  
29 510.5 22.1 198 4 US-10-293-832-33 Sequence 33, Appl  
30 236.5 10.2 273 4 US-10-186-180-15 Sequence 15, Appl  
31 234.5 10.1 273 4 US-10-186-180-14 Sequence 14, Appl  
32 233.5 10.1 220 3 US-09-925-055D-19 Sequence 19, Appl  
33 233.5 10.1 220 4 US-10-807-837-44 Sequence 44, Appl  
34 233.5 10.1 273 4 US-10-186-180-2 Sequence 2, Appl  
35 233.5 10.1 273 4 US-10-358-228-8 Sequence 8, Appl  
36 233.5 10.1 476 3 US-09-925-055D-23 Sequence 23, Appl  
37 233.5 10.1 476 4 US-10-104-919-62 Sequence 62, Appl  
38 233.5 10.1 476 4 US-10-395-741B-63 Sequence 63, Appl  
39 233.5 10.1 476 5 US-10-968-432-62 Sequence 62, Appl  
40 232.5 10.1 273 4 US-10-186-180-16 Sequence 16, Appl  
41 228.5 9.9 325 3 US-09-870-574-3 Sequence 3, Appl  
42 228.5 9.9 325 3 US-09-949-192-5 Sequence 5, Appl  
43 228.5 9.9 325 4 US-10-052-586-390 Sequence 390, App  
44 228.5 9.9 325 4 US-10-066-500-137 Sequence 137, App  
45 228.5 9.9 325 4 US-10-174-590-390 Sequence 390, App

#### ALIGNMENTS

#### RESULT 1

US-09-240-675-2

; Sequence 2, Application US/09240675

; Patent No. US20020055492A1

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick

; APPLICANT: MEYER, Francois

; APPLICANT: MAGUIRE, Deborah

; APPLICANT: PLAVEC, Ivan

; APPLICANT: TOVEY, Michael G.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/240,675

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/307,588

; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: PCT/EP93/00770

; FILING DATE: 30-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 92400902.0

; FILING DATE: 31-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: SAXE, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 17283/117/GUPL

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 436 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-240-675-2

Query Match 100.0%; Score 2313; DB 3; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESNGVT 60

Qy 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120

Qy 121 TPRKQAGIPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
Db 121 TPRKQAGIPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180

Qy 181 ENIYSRHKIYKLSPEPTYCLKVAALITTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLKVAALITTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240

Qy 241 NONVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360

Qy 361 VIQDYPLIYIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 2  
US-10-824-981-2  
; Sequence 2, Application US/10824981  
; Publication No. US20040191840A1  
; GENERAL INFORMATION:  
; APPLICANT: Benoît, Patrick  
; APPLICANT: Maguire, Deborah  
; APPLICANT: Plavec, Ivan  
; APPLICANT: Tovy, Michael  
; APPLICANT: Meyer, Francois  
; TITLE OF INVENTION: Monoclonal Antibodies Against The Interferon Receptor, With  
; FILE REFERENCE: A-72230-2  
; CURRENT APPLICATION NUMBER: US/10/824,981  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US 09/240,675  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: US 08/307,588  
; PRIOR FILING DATE: 1994-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP93/00770  
; PRIOR FILING DATE: 1993-03-30  
; PRIOR APPLICATION NUMBER: EP 92400902.0  
; PRIOR FILING DATE: 1992-03-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-824-981-2

Query Match 100.0%; Score 2313; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESNGVT 60

Qy 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120

Qy 121 TPRKQAGIPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180  
Db 121 TPRKQAGIPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWNSSGVEERI 180

Qy 181 ENIYSRHKIYKLSPEPTYCLKVAALITTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLKVAALITTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240

Qy 241 NONVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVVLKWDYTYANMTFQVWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
Db 301 GIYLLRVOASDGNNTSPWSEIEKFDTEIOAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360

Qy 361 VIQDYPLIYIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYIIFWNTSNAERKIIIEKTDVTPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 3  
US-10-473-127-1756  
; Sequence 1756, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1756  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1756

Query Match 100.0%; Score 2313; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWLSAAAGGNLKSQKVEVDIIDDNFILRNRSDESNGVT 60

Qy 61 FSDYQKTGMNDWIKLSGCQNTSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEDSF 120

Db 61 FSDYQKTGMDNWIKLSCQNTTSTKCNFSSLLKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Qy 181 ENISYRHKIYKLSPTTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENISYRHKIYKLSPTTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NONVYLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVYLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRQVQSDGNTSFWSEBEIKEDTEIQAELLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
Db 301 GIYLLRQVQSDGNTSFWSEBEIKEDTEIQAELLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNARKEIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 4

US-10-473-127-1758  
; Sequence 1758, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1758  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1758

Query Match 100.0%; Score 2313; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
Qy 61 FSDYQKTGMDNWIKLSCQNTTSTKCNFSSLLKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMDNWIKLSCQNTTSTKCNFSSLLKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180

Qy 181 ENISYRHKIYKLSPTTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENISYRHKIYKLSPTTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NONVYLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVYLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRQVQSDGNTSFWSEBEIKEDTEIQAELLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
Db 301 GIYLLRQVQSDGNTSFWSEBEIKEDTEIQAELLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNARKEIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNARKEIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 5

US-10-473-127-1764  
; Sequence 1764, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1764  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1764

Query Match 100.0%; Score 2313; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3.6e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILNRNRSDESIGNVT 60  
Qy 61 FSDYQKTGMDNWIKLSCQNTTSTKCNFSSLLKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMDNWIKLSCQNTTSTKCNFSSLLKLVNVEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEADKAIVIHISPTKDSVNMWALDGLSFTYSLLIWKNSGVEERI 180  
Qy 181 ENISYRHKIYKLSPTTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Db 181 ENISYRHKIYKLSPTTYCLVKVKAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
Qy 241 NONVYLKWDYTYANMTFQVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300

Db 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRVQASDGNNTSFWSBEEKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

Db 301 GIYLLRVQASDGNNTSFWSBEEKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

Qy 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Db 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436

Db 421 FSDAVCEKTKPGNTSK 436

RESULT 6

US-09-240-675-4

; Sequence 4, Application US/09240675

; Patent No. US20020055492A1

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick

; APPLICANT: MEYER, Francois

; APPLICANT: MAGUIRE, Deborah

; APPLICANT: FLAVEC, Ivan

; APPLICANT: TOVEY, Michael G.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

; TITLE OF INVENTION: INTERFERON

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA: US/09/240,675

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/307,588

; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: PC/EP93/00770

; FILING DATE: 30-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 92400902.0

; FILING DATE: 31-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: SAXE, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 17283/117/GUPL

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-240-675-4

Query Match 100.0%; Score 2313; DB 3; Length 557;

Best Local Similarity 100.0%; Pred. No. 5e-196;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNWRSDESQVNT 60

Db 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNWRSDESQVNT 60

Qy 61 FSPDYOKTGMNDWIKLSGCCQNTITSTKCNFSSSLKNVYEEIKLIRAEKENTSSWYEVDSF 120

Db 61 FSPDYOKTGMNDWIKLSGCCQNTITSTKCNFSSSLKNVYEEIKLIRAEKENTSSWYEVDSF 120

Qy 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180

Db 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180

Qy 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCHIKTTVENELPPPENIEVSQ 240

Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCHIKTTVENELPPPENIEVSQ 240

Qy 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

Db 241 NQNVLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRVQASDGNNTSFWSBEEKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

Db 301 GIYLLRVQASDGNNTSFWSBEEKFDETEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

Qy 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Db 361 VIQDYPLIYELIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436

Db 421 FSDAVCEKTKPGNTSK 436

RESULT 7

US-10-358-228-3

; Sequence 3, Application US/10358228

; Publication No. US20030211578A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Interferon Receptor HKAEF92

; FILE REFERENCE: PF465C1

; CURRENT APPLICATION NUMBER: US/10/358,228

; CURRENT FILING DATE: 2003-02-05

; PRIOR APPLICATION NUMBER: 09/453,569

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: 09/326,216

; PRIOR FILING DATE: 1999-06-03

; PRIOR APPLICATION NUMBER: 60/088,185

; PRIOR FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 557

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-358-228-3

Query Match 100.0%; Score 2313; DB 4; Length 557;

Best Local Similarity 100.0%; Pred. No. 5e-196;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNWRSDESQVNT 60

Db 1 MMVLLGATTLVLVAVGFWLVAAGGKLNKSPQKVEVDIIDNFILRNWRSDESQVNT 60

Qy 61 FSPDYOKTGMNDWIKLSGCCQNTITSTKCNFSSSLKNVYEEIKLIRAEKENTSSWYEVDSF 120

Db 61 FSPDYOKTGMNDWIKLSGCCQNTITSTKCNFSSSLKNVYEEIKLIRAEKENTSSWYEVDSF 120

Qy 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180

Db 121 TPFRKAQIGPPEVHLEAEKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180

Qy 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCHIKTTVENELPPPENIEVSQ 240

Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGYSPVHCHIKTTVENELPPPENIEVSQ 240

Qy 241 NONTYVLKWDYTYANNMTFOVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONTYVLKWDYTYANNMTFOVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Qy 421 PSDAVCEKTKPGNTSK 436  
Db 421 PSDAVCEKTKPGNTSK 436

## RESULT 8

US-10-473-127-1757  
; Sequence 1757, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1757  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1757

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGNKLSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNKLSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Qy 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPVHLEAEDKAVIHISPTGKDSVMWALDGLSFTYSLIWKNSSGVEERI 180  
Db 121 TPFRKAQIGPPVHLEAEDKAVIHISPTGKDSVMWALDGLSFTYSLIWKNSSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
Qy 241 NONTYVLKWDYTYANNMTFOVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONTYVLKWDYTYANNMTFOVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420

Db 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Qy 421 PSDAVCEKTKPGNTSK 436  
Db 421 PSDAVCEKTKPGNTSK 436

## RESULT 9

US-10-473-127-1759  
; Sequence 1759, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1759  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1759

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGNKLSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGNKLSPOKVEVDIIDDNPFILRNRSDESQVNT 60  
Qy 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
Qy 121 TPFRKAQIGPPVHLEAEDKAVIHISPTGKDSVMWALDGLSFTYSLIWKNSSGVEERI 180  
Db 121 TPFRKAQIGPPVHLEAEDKAVIHISPTGKDSVMWALDGLSFTYSLIWKNSSGVEERI 180  
Qy 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQ 240  
Qy 241 NONTYVLKWDYTYANNMTFOVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONTYVLKWDYTYANNMTFOVWLHAFLEKRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQK 300  
Qy 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Db 301 GIYLLRVQASDGNNTSFWSBEIKFDTETQAFLLPPVFNIRSLDSFHIYIGAPKQSGNTP 360  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTVPNLKPLTYVCVKARAHMTWDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 10  
US-10-473-127-1760  
; Sequence 1760, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1760  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1760

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60

Qy 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120

Qy 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Db 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180

Qy 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240

Qy 241 NONVVLKWDVYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVVLKWDVYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360  
Db 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360

Qy 361 VIQDYPLIYIIIFWENTSNARKEIIIEKTDVTVPNLKPLTVYCVKAAHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYIIIFWENTSNARKEIIIEKTDVTVPNLKPLTVYCVKAAHTMDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 12  
US-10-473-127-1765  
; Sequence 1765, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.

RESULT 11  
US-10-473-127-1763  
; Sequence 1763, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1763  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1763

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60  
Db 1 MMVLLGATTLVLVAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60

Qy 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120  
Db 61 FSDYQKTGMDNWKLSGCCNITSTKCNFSSKLNVYEEIKLRIRAEKENTSSWYEDSF 120

Qy 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180  
Db 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERI 180

Qy 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGYSPVHCITKTVENELPPPENIEVSQ 240

Qy 241 NONVVLKWDVYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFQK 300  
Db 241 NONVVLKWDVYANMTFQVQWLHAFKRNPNHLYKWQIPDCENVKTTQCVFPQNVFQK 300

Qy 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360  
Db 301 GIYLLRQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHIYIGAPQSGNTP 360

Qy 361 VIQDYPLIYIIIFWENTSNARKEIIIEKTDVTVPNLKPLTVYCVKAAHTMDEKLNKSSV 420  
Db 361 VIQDYPLIYIIIFWENTSNARKEIIIEKTDVTVPNLKPLTVYCVKAAHTMDEKLNKSSV 420

Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1765  
; LENGTH: 557  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-473-127-1765

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLLVAVGPWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVGNT 60  
DB 1 MMVLLGATTLLVAVGPWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVGNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEDSF 120  
QY 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
DB 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
QY 241 NONVYLKWDYTYANNMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 NONVYLKWDYTYANNMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSEIEKFDTEIOAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSEIEKFDTEIOAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 13  
US-10-473-127-1766  
; Sequence 1766, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1766  
; LENGTH: 557  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-473-127-1766

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLLVAVGPWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVGNT 60  
DB 1 MMVLLGATTLLVAVGPWLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESVGNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNITSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEDSF 120  
QY 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
DB 121 TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLIWKNSGVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
QY 241 NONVYLKWDYTYANNMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
DB 241 NONVYLKWDYTYANNMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
QY 301 GIYLLRVQASDGNNTSFWSEIEKFDTEIOAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
DB 301 GIYLLRVQASDGNNTSFWSEIEKFDTEIOAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWNTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 14  
US-10-473-127-1772  
; Sequence 1772, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026WO1  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01

; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1772  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1772

Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVLLGATTLLVAVGFWLVSAAAGGKNLSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
Db 1 MMVLLGATTLLVAVGFWLVSAAAGGKNLSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
  
Qy 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSF 120  
  
Qy 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
  
Qy 181 ENIYSRHKIYKLSPEITTYCLVKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEITTYCLVKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
  
Qy 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
  
Qy 301 GIYLLRQVQSDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
Db 301 GIYLLRQVQSDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHMTMDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHMTMDEKLNKSSV 420  
  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 15  
US-10-473-127-1773  
; Sequence 1773, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1773  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1773  
  
Query Match 100.0%; Score 2313; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 5e-196;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVLLGATTLLVAVGFWLVSAAAGGKNLSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
Db 1 MMVLLGATTLLVAVGFWLVSAAAGGKNLSPQKVEVDIIDDNFILRNRSDES VGNVT 60  
  
Qy 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSF 120  
Db 61 FSPDYQKTGMNDWIKLSCQNITSTKCNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSF 120  
  
Qy 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
  
Qy 181 ENIYSRHKIYKLSPEITTYCLVKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPEITTYCLVKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
  
Qy 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NONVYLKWDYTYANMTFQVQWLHAFKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
  
Qy 301 GIYLLRQVQSDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
Db 301 GIYLLRQVQSDGNNTSFWSBEIKFDETEIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTP 360  
  
Qy 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHMTMDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHMTMDEKLNKSSV 420  
  
Qy 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436

Search completed: January 17, 2006, 07:35:29  
Job time : 89.5544 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:19:53 ; Search time 17.7109 Seconds  
(without alignments)  
232.741 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVLLGATTLVLVAGPWV.....KSSVFSDAVCBKTKPNTSK 436

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/prodata/2/pubpaa/US08 NEW PUB.pep:  
2: /cgn2\_6/prodata/2/pubpaa/US06 NEW PUB.pep:  
3: /cgn2\_6/prodata/2/pubpaa/US07 NEW PUB.pep:  
4: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW PUB.pep:  
5: /cgn2\_6/prodata/2/pubpaa/US09 NEW PUB.pep:  
6: /cgn2\_6/prodata/2/pubpaa/US10 NEW PUB.pep:  
7: /cgn2\_6/prodata/2/pubpaa/US11 NEW PUB.pep:  
8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200	8.6	542	6	US-10-131-826A-188
2	198	8.6	553	6	US-10-636-716-2
3	198	8.6	553	6	US-10-636-716-14
4	198	8.6	553	6	US-10-636-716-16
5	198	8.6	553	6	US-10-636-716-18
6	198	8.6	553	6	US-10-636-716-20
7	198	8.6	553	6	US-10-636-716-22
8	198	8.6	553	6	US-10-636-716-24
9	198	8.6	553	6	US-10-636-716-26
10	198	8.6	553	6	US-10-636-716-28
11	198	8.6	553	6	US-10-636-716-30
12	198	8.6	553	6	US-10-636-716-32
13	198	8.6	553	6	US-10-636-716-34
14	198	8.6	553	6	US-10-636-716-36
15	198	8.6	553	6	US-10-636-716-38
16	198	8.6	553	6	US-10-636-716-40
17	198	8.6	553	6	US-10-636-716-42
18	198	8.6	553	6	US-10-636-716-44
19	198	8.6	553	6	US-10-636-716-46
20	198	8.6	553	6	US-10-636-716-48
21	174.5	7.5	221	6	US-10-636-716-56
22	169.5	7.3	221	6	US-10-636-716-54
23	168.5	7.3	221	6	US-10-636-716-50
24	168.5	7.3	384	7	US-11-075-351-12
25	168.5	7.3	404	7	US-11-075-351-23

26	168.5	7.3	404	7	US-11-075-351-25
27	167.5	7.2	221	6	US-10-636-716-52
28	165.5	7.2	221	6	US-10-636-716-60
29	162.5	7.0	221	6	US-10-636-716-58
30	151.5	6.5	366	7	US-11-075-351-38
31	151	6.5	574	7	US-11-102-240-164
32	149.5	6.5	374	7	US-11-075-351-42
33	147.5	6.4	311	6	US-10-131-826A-32
34	147.5	6.4	311	6	US-10-512-214-16
35	123	5.3	522	7	US-11-184-399-8
36	118	5.1	1005	7	US-11-113-424-63
37	117.5	5.1	2214	7	US-11-080-991-94
38	115	5.0	244	7	US-11-184-399-10
39	115	5.0	473	7	US-11-165-141-23
40	115	5.0	520	7	US-11-098-662-12
41	115	5.0	520	7	US-11-165-141-19
42	115	5.0	599	7	US-11-165-141-33
43	109	4.7	203	7	US-11-165-141-4
44	109	4.7	491	7	US-11-098-662-14
45	109	4.7	491	7	US-11-165-141-2

ALIGNMENTS

RESULT 1  
US-10-131-826A-188  
; Sequence 188, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P333030R1C128  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.



TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-14

Query Match 8.6%; Score 198; DB 6; Length 553;  
Best Local Similarity 21.0%; Pred. No. 1.1e-09;  
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;  
QY 11 LVLVAVGPW--VLSAAGGKNLSPQKVEVDIIDNFILRNWRSDESVG-NVTFSPDYQK 67  
DB 18 LLLLLAAPGRAWPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75  
QY 68 TGMNDWIKLGGQNTITSTKCNFSSLLKNVVEIKLRIRA-EKENTSSWYEVDSFTPRKA 126  
DB 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKCKWAESGRFPFLET 135  
QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMWALDGLSFTYSILLIWNSSGVE 177  
DB 136 QIGPPEVALTTDEKISVSVLTAPKWKRPEDLPVSMQOIYSLNKNVSVLNTKSNRTWS 195  
QY 178 ERNIYSRHKIYK--LSPETTYCLKVAALITSWKIGYSPVHCITKTVENE-----228  
DB 196 QCVTN---HTVLVLTWLEPNTLYCVHVESFVPPPPRAQPSKQCARTLKQDSSEPKAKI 251  
QY 229 -----LPPNTEVSVQNYVNLKWDYTYANMTFQV-QWLHAFKRNPGNHLKWKQIPD 282  
DB 252 IFWYVLP-----ISITY-----FLFSVMGYSIYRYIHVGKXHPANLI-----289  
QY 283 CENVKTTQCVFQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDTETI---QAFLLPPVENI 339  
DB 290 -----LIVGNEFKRFFV-----PAEKIVINFITLMSDDSKSHQDMSLLGKSDV 336  
QY 340 RSLSDSFHVIYIGAPKQSGNTPVIQDYPLIVEI-----IFWNTSNAERKIIIEKKTDV 391

DB 337 SSLND-----POPSGNLRPPQBEERVKHILGYASHLMWEIFCDSEENTEGTSFTQBSL 388  
QY 392 --TVPNLKLPLTVY 402  
DB 389 SRTIPDPKTVIEY 401  
RESULT 4  
US-10-636-716-16  
Sequence 16, Application US/10636716  
Publication No. US20050244832A9  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelnberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrish, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc. East  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/636,716  
FILING DATE: 07-AUG-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-10-636-716-16

Query Match 8.6%; Score 198; DB 6; Length 553;  
Best Local Similarity 21.0%; Pred. No. 1.1e-09;  
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;  
QY 11 LVLVAVGPW--VLSAAGGKNLSPQKVEVDIIDNFILRNWRSDESVG-NVTFSPDYQK 67  
DB 18 LLLLLAAPGRAWPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75  
QY 68 TGMNDWIKLGGQNTITSTKCNFSSLLKNVVEIKLRIRA-EKENTSSWYEVDSFTPRKA 126  
DB 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTKCKWAESGRFPFLET 135



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; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-20

```

```

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGKLNKSPQKVEVDIIDNFILRNWRSDESVG-NVTFSPDYOK 67
Db 18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSNKKNVLQWTPPEGLQGVKVTYTVQYFI 75

QY 68 TGMNDNWKLSGCONITSTKCNFSSKLNVYBEIKLRIRA-EKENTSSWYEVDSFTPFKA 126
Db 76 YQKKWLKSECRNIRTYCDLSAETSDYEHQYAKVKAIMGTKCKWAESGRFYPFLET 135

QY 127 QIGPPEVHLEADKAIVIHISGKTK-----DSVMWALDGLSFTYSLLIWKSSGVE 177
Db 136 QIGPPEVALTTDEKSISVVLTAPEKWKRNPELPSVMOQIYSNLKNVSVLNTKSNRTWS 195

QY 178 ERIENIYSHKIYK--LSPETTYCLVKVKAALLTSMKIGVYSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLENTLYCVHVESFVPGPPRAQPSKQKARTLKQSSSEFKAKI 251

QY 229 -----LPPPENIEVSQNVQNYVLKWDYTYANMTFQV-OMLHAFLEKRNPGNHLKYWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIVRYIHVGKEXHPANLI----- 289

QY 283 CENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSFWSBEIKFDTEI---OAFLLPPVFN 339
Db 290 -----LIYGNEDFKRFV---PAEKIVINFITLNSDDSKISHQDMSLLGKSSDV 336

QY 340 RLSDSFHIYIGAPKQSGNTPVQIDYPLIYEI-----IFWENTSNAERKIEKKTVD 391
Db 337 SSLND-----POPSGNLRPPQBEVEVKHLYASHLMEIFCDSBENTGTSFTQOESL 388

QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

```

```

RESULT 7
US-10-636-716-22
; Sequence 22, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jernberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR

```

```

; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-22

```

```

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGKLNKSPQKVEVDIIDNFILRNWRSDESVG-NVTFSPDYOK 67
Db 18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSNKKNVLQWTPPEGLQGVKVTYTVQYFI 75

QY 68 TGMNDNWKLSGCONITSTKCNFSSKLNVYBEIKLRIRA-EKENTSSWYEVDSFTPFKA 126
Db 76 YQKKWLKSECRNIRTYCDLSAETSDYEHQYAKVKAIMGTKCKWAESGRFYPFLET 135

QY 127 QIGPPEVHLEADKAIVIHISGKTK-----DSVMWALDGLSFTYSLLIWKSSGVE 177
Db 136 QIGPPEVALTTDEKSISVVLTAPEKWKRNPELPSVMOQIYSNLKNVSVLNTKSNRTWS 195

QY 178 ERIENIYSHKIYK--LSPETTYCLVKVKAALLTSMKIGVYSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLENTLYCVHVESFVPGPPRAQPSKQKARTLKQSSSEFKAKI 251

QY 229 -----LPPPENIEVSQNVQNYVLKWDYTYANMTFQV-OMLHAFLEKRNPGNHLKYWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIVRYIHVGKEXHPANLI----- 289

QY 283 CENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSFWSBEIKFDTEI---OAFLLPPVFN 339
Db 290 -----LIYGNEDFKRFV---PAEKIVINFITLNSDDSKISHQDMSLLGKSSDV 336

QY 340 RLSDSFHIYIGAPKQSGNTPVQIDYPLIYEI-----IFWENTSNAERKIEKKTVD 391
Db 337 SSLND-----POPSGNLRPPQBEVEVKHLYASHLMEIFCDSBENTGTSFTQOESL 388

```

```
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDKTVIEY 401

RESULT 8
US-10-636-716-24
; Sequence 24, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-24

Query Match 8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGKGLKSPQKVEVDIIDDNFILRNWRSDSVG-NVTFSPDYQK 67
Db 18 LLLLAAPWGRAPVCVSGG--LPKPANITFUSINMKNVLQWTPPEGQGVKVTYVQFFI 75
QY 68 TGMNDWIKLSCQNTITKCNFSSILKNVYEEIKLIRRA-EKENTSSWYEDVSTPFRKA 126
Db 76 YGQKKWLKNSCRNIRNYCDLSAETSDYEHQYAKVKAIWGTCRKAWSGRYPFLET 135
QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMWALDGLSFTYSLIWNSSGOVE 177

Db 136 QIGPPEVALTTDEKSIISVLTAPKWKRNKPNBDLPVSMQOIYSNLKYNVSLMTKSNRTWS 195
QY 178 ERIENIYSRHKIYK--LSPETTYCLVKVKAALLTSWKIGVYSPVHCITKTVE----- 228
Db 196 QCVTN-----HTLVLTWLEPNLYCVHVESFVPGPRRAQPSKQKQARTLKQOSSSEFKAKI 251
QY 229 -----LPPPENIEVSVQNYVNLKWDYTYANMTFQV-QWLHAFILKRNFGNHLKWKQIPD 282
Db 252 IFWVVLV-----ISITV-----FLFSVMGYSIYRYIHVGKEKHPANLI----- 289
QY 283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSBEIKFDTEI-----QAFLLPVPVNI 339
Db 290 -----LIYGNFDFKRFV-----PAEKIVINFITLINISDDSKISHQDMSLLGKSSDV 336
QY 340 RSLSDSFHIYIGAPKQSNTPVIODYPLIYEI-----IFWENTSNAERKILIEKKTVDV 391
Db 337 SSLND-----FQPSGNLRPPQEBEVEVKHLGYASHLMEIFCDSEENTEGETSFTQOBSL 388
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDKTVIEY 401

RESULT 9
US-10-636-716-26
; Sequence 26, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-26

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGNLKSPQKVEVDIIDDNFILRNRSRDSVG-NVTFSFDYQK 67
Db 18 LLLLLAAPGWRAPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
QY 68 TGMNDWIKLGGCONITSTKCNFSSKLNVYEEIKLIRA-EKENTSSWEVDSFTPRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTCCKWAESGRFYFPLET 135
QY 127 QIGPPVHLEADKATVIHISPTK-----DSVMWALDGLSFTYSLLIWNSSGVE 177
Db 136 QIGPPEVALTTDEKSISSVLTAPKWKRNPEDLPSVMOQIYSLNLYNVSVLNKSRTWS 195
QY 178 ERIENIYSRHKIYK--LSPETTYCLVKKAALLTSWKIGVSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLENTLYCVHVSFVPGPPRAQSEKQCARTLKQSSSEFKAKI 251
QY 229 -----LPPENIEVSQONQYVLKWDYTYANMTFQV-OMLHAFKRNPGNHLKYWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRVIVHGKXHPANLI----- 289
QY 283 CENVKTTQCVPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDEI---QAFLLPPVFN 339
Db 290 -----LYGNEFDKRFV---PAEKIVINFTILNISDDSKISHQDMSLLGKSDV 336
QY 340 RSLSDSFHIYIGAPKQSGNTPTVIQDYPLIYEI-----IFWENTSNAERKIIIEKTDV 391
Db 337 SSLND-----PQSGNLRPQEEEVKHLGYASHLMEIFCDSENTGTSFTQOESL 388
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 11
US-10-636-716-30
; Sequence 30, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.1e-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSAAGGNLKSPQKVEVDIIDDNFILRNRSRDSVG-NVTFSFDYQK 67
Db 18 LLLLLAAPGWRAPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
QY 68 TGMNDWIKLGGCONITSTKCNFSSKLNVYEEIKLIRA-EKENTSSWEVDSFTPRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVAIWGTCCKWAESGRFYFPLET 135
QY 127 QIGPPVHLEADKATVIHISPTK-----DSVMWALDGLSFTYSLLIWNSSGVE 177
Db 136 QIGPPEVALTTDEKSISSVLTAPKWKRNPEDLPSVMOQIYSLNLYNVSVLNKSRTWS 195
QY 178 ERIENIYSRHKIYK--LSPETTYCLVKKAALLTSWKIGVSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLENTLYCVHVSFVPGPPRAQSEKQCARTLKQSSSEFKAKI 251
QY 229 -----LPPENIEVSQONQYVLKWDYTYANMTFQV-OMLHAFKRNPGNHLKYWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRVIVHGKXHPANLI----- 289
QY 283 CENVKTTQCVPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDEI---QAFLLPPVFN 339
Db 290 -----LYGNEFDKRFV---PAEKIVINFTILNISDDSKISHQDMSLLGKSDV 336
QY 340 RSLSDSFHIYIGAPKQSGNTPTVIQDYPLIYEI-----IFWENTSNAERKIIIEKTDV 391
Db 337 SSLND-----PQSGNLRPQEEEVKHLGYASHLMEIFCDSENTGTSFTQOESL 388
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 11
US-10-636-716-30
; Sequence 30, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60

COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/636,716
FILING DATE: 07-AUG-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
```

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/636,716
/ FILING DATE: 07-AUG-2003
/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/
/ US-10-636-716-30
/
/ Query Match 8.6%; Score 198; DB 6; Length 553;
/ Best Local Similarity 21.0%; Pred. No. 1.1e-09;
/ Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;
/
/ QY 11 LVLVAVGPW--VLSAAGGNLKSPOKVEVDIIDNFILRNWRSDESVG-NVTFSEFDYQK 67
/ Db 18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLOMTPEGLQGVKVTYTVQVPI 75
/
/ QY 68 TGMNWKLSGQNTITSTKCNFSSLLKLVYBEIKLIRA-EKENTSSWYVDSTFPPFKA 126
/ Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAINGTKCSKWAESGRFYPFLET 135
/
/ QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMWALDGLSFTYSLLIWKNSSGVE 177
/ Db 136 QIGPPEVALTTDEKISVVLTAPEKRNPELPSVMQIYSLNLYNVLNKSNTKSNRTWS 195
/
/ QY 178 ERIENIYSHKIYK--LSPETTYCLKVAALTSWKIGVYSPVHCITVENE----- 228
/ Db 196 QCVTN-----HTLVLTWLEPNTLYCVHVSFVPGPPRAQPSKQKARTLKQSSBFKAKI 251
/
/ QY 229 -----LPPPENIEVSQNVYLVKWDYTYANNTFQV-QWLHAFLLKRNPNHLYKWKQIPD 282
/ Db 252 IFWYVLP-----ISITV-----FLPSVMGYSIYRIYHVHGEKHPANLI----- 289
/
/ QY 283 CENVKTCQVPQNVQFGKIYLLRVOASDGNNTSPWSEIEKPDTEI---QAFLLPPVFN 339
/ Db 290 -----LIYGNEDKRFV---PAEKIVINFTILNISDSKISHQDMSLLGKSDV 336
/
/ QY 340 RSLSDSFHYIGAPKQSGNTVPIDYPLIYEI-----IFWENTSNAERKLIBKKTVDV 391
/ Db 337 SSLND-----POPSGNLRNPQBEIEVKHLYGASHLMEIFCDSEENTGTSFTQBSL 388
```

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QY 392 --TVENLKPLTVY 402
/
/ Db 389 SRTIPDPKTVIEY 401
/
/ RESULT 12
/ US-10-636-716-32
/ Sequence 32, Application US/10636716
/ Publication No. US20050244832A9
/ GENERAL INFORMATION:
/ APPLICANT: Lok, Si
/ APPLICANT: Kho, Choon J.
/ APPLICANT: Jelmsberg, Anna C.
/ APPLICANT: Adams, Robyn L.
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Farrah, Theresa M.
/ TITLE OF INVENTION: CYTOKINE RECEPTOR
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSEQ for Windows Version 2.0
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/636,716
/ FILING DATE: 07-AUG-2003
/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/
/ US-10-636-716-32
/
/ Query Match 8.6%; Score 198; DB 6; Length 553;
/ Best Local Similarity 21.0%; Pred. No. 1.1e-09;
/ Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;
/
/ QY 11 LVLVAVGPW--VLSAAGGNLKSPOKVEVDIIDNFILRNWRSDESVG-NVTFSEFDYQK 67
/ Db 18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLOMTPEGLQGVKVTYTVQVPI 75
/
/ QY 68 TGMNWKLSGQNTITSTKCNFSSLLKLVYBEIKLIRA-EKENTSSWYVDSTFPPFKA 126
/ Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAINGTKCSKWAESGRFYPFLET 135
/
/ QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMWALDGLSFTYSLLIWKNSSGVE 177
/ Db 136 QIGPPEVALTTDEKISVVLTAPEKRNPELPSVMQIYSLNLYNVLNKSNTKSNRTWS 195
/
/ QY 178 ERIENIYSHKIYK--LSPETTYCLKVAALTSWKIGVYSPVHCITVENE----- 228
/ Db 196 QCVTN-----HTLVLTWLEPNTLYCVHVSFVPGPPRAQPSKQKARTLKQSSBFKAKI 251
/
/ QY 229 -----LPPPENIEVSQNVYLVKWDYTYANNTFQV-QWLHAFLLKRNPNHLYKWKQIPD 282
/ Db 252 IFWYVLP-----ISITV-----FLPSVMGYSIYRIYHVHGEKHPANLI----- 289
/
/ QY 283 CENVKTCQVPQNVQFGKIYLLRVOASDGNNTSPWSEIEKPDTEI---QAFLLPPVFN 339
/ Db 290 -----LIYGNEDKRFV---PAEKIVINFTILNISDSKISHQDMSLLGKSDV 336
/
/ QY 340 RSLSDSFHYIGAPKQSGNTVPIDYPLIYEI-----IFWENTSNAERKLIBKKTVDV 391
/ Db 337 SSLND-----POPSGNLRNPQBEIEVKHLYGASHLMEIFCDSEENTGTSFTQBSL 388
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Db 136 QIGPPEVALTTDEKISVVLTAPEKWKRNPEDLFVSMQOIIYSLKYNVSVLNTKSNRTWS 195
Qy 178 ERIENIYSRHKIYK--LSPETTYCLVKVKAALLTSWKIGVYSPVHCICKTTVENE----- 228
Db 196 QCVTN---HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCAKTLKQOSSEFKAKI 251
Qy 229 -----LPPENIEVSQNONVYLKWDYTYANMTFQV-OMLHAPLKRPNHLYKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRIYHVGEKHPANLI----- 289
Qy 283 CENVKTTQCVPFQKGIYLLRVQASDGNNTSFWESEIKPDEI---QAFLLPPVFN 339
Db 290 -----LIYNEEDKRFV---PAEKIVINFITLNSDDSKISHQDMSLLGKSSDV 336
Qy 340 RSLSDSFHIYIGAPKOSGNTPTQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQSGNLRRPQEEVEVKHLYASHLMEIFCDSEBTEGTSFTQOESL 388
Qy 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 13
US-10-636-716-34
; Sequence 34, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

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; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-10-636-716-34

Query Match 8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.le-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

Qy 11 LVLVAVGPM--VLSAAGGKNLKSPQKVEVDIIDNFILRNRSDESUG-VNTFSDYQK 67
Db 18 LLLLLAAPGRAWPCVSGG--LPKANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
Qy 68 TGMNDWIKSLGCONITSTKCNFSSLLKLVYEELKLRIRA-EKENTSSWYEDVSFTPRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDEYHQYAKVKAIWGTKCSKWAESGRFYPLET 135
Qy 127 QIGPPRHVLEARDKATVIHISPTK-----DSVMWALDGLSFTYSLLIWNSSGVE 177
Db 136 QIGPPEVALTTDEKISVVLTAPEKWKRNPEDLFVSMQOIIYSLKYNVSVLNTKSNRTWS 195
Qy 178 ERIENIYSRHKIYK--LSPETTYCLVKVKAALLTSWKIGVYSPVHCICKTTVENE----- 228
Db 196 QCVTN---HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCAKTLKQOSSEFKAKI 251
Qy 229 -----LPPENIEVSQNONVYLKWDYTYANMTFQV-OMLHAPLKRPNHLYKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----FLFSVMGYSIYRIYHVGEKHPANLI----- 289
Qy 283 CENVKTTQCVPFQKGIYLLRVQASDGNNTSFWESEIKPDEI---QAFLLPPVFN 339
Db 290 -----LIYNEEDKRFV---PAEKIVINFITLNSDDSKISHQDMSLLGKSSDV 336
Qy 340 RSLSDSFHIYIGAPKOSGNTPTQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQSGNLRRPQEEVEVKHLYASHLMEIFCDSEBTEGTSFTQOESL 388
Qy 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 14
US-10-636-716-36
; Sequence 36, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-36

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.le-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSSAAGGKNLSPQKVEVDIIDNFILRWNRSDSVG-NVTFSPDYQK 67
Db 18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSNMKNVLQWTPPEGLQGVKVTYTVQYPI 75
QY 68 TGMNDWIKLGGQNTSTKCNFSSKLNVYBEIKLIRA-EKENTSSWYVDSTPPFRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCSCWAESGRFYPPLET 135
QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMALDGLSTYSLLIWKNSSGVE 177
Db 136 QIGPPEVALTTDEKSIISVLTAPKWKRNPELPSVSMQOIYSNLKNVSVLNTKSNRTWS 195
QY 178 ERIENIYSRHKYK--LSPETTYCLKVKKAALLTSWKIGVYSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARLTKDOSSEFKAKI 251
QY 229 -----LPPPENIEVSQNTYLVKWDYTYANNTFOV-OWLHAFILKRNPNHLYKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----PLFSVMGYSIYRIVHVGKEKHPANLI----- 289
QY 283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEIEKPDTEI---QAFLLPPVFN 339
Db 290 -----LIYGNFEDKRFV----PAEKIVINFTILNISDDSKISHQMSLLGKSSDV 336
QY 340 RSLSDSFHIYGAPKQSGNTPIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQPSGNLRPPQEEVVKHLYGASHLMELIFCDSEENTEGTSFTQESL 388
QY 392 --TVPNLKPLTVY 402
Db 389 SRTIPDPKTVIEY 401

RESULT 15
US-10-636-716-38
; Sequence 38, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-38

```

```

Query Match      8.6%; Score 198; DB 6; Length 553;
Best Local Similarity 21.0%; Pred. No. 1.le-09;
Matches 91; Conservative 79; Mismatches 173; Indels 90; Gaps 17;

QY 11 LVLVAVGPW--VLSSAAGGKNLSPQKVEVDIIDNFILRWNRSDSVG-NVTFSPDYQK 67
Db 18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSNMKNVLQWTPPEGLQGVKVTYTVQYPI 75
QY 68 TGMNDWIKLGGQNTSTKCNFSSKLNVYBEIKLIRA-EKENTSSWYVDSTPPFRKA 126
Db 76 YGQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCSCWAESGRFYPPLET 135
QY 127 QIGPPEVHLEADKAIVIHISPGTK-----DSVMALDGLSTYSLLIWKNSSGVE 177
Db 136 QIGPPEVALTTDEKSIISVLTAPKWKRNPELPSVSMQOIYSNLKNVSVLNTKSNRTWS 195
QY 178 ERIENIYSRHKYK--LSPETTYCLKVKKAALLTSWKIGVYSPVHCIKTTVENE----- 228
Db 196 QCVTN-----HTLVLTWLEPNTLYCVHVESFVGPFPRAQPSKQCARLTKDOSSEFKAKI 251
QY 229 -----LPPPENIEVSQNTYLVKWDYTYANNTFOV-OWLHAFILKRNPNHLYKWKQIPD 282
Db 252 IFWYVLP-----ISITV-----PLFSVMGYSIYRIVHVGKEKHPANLI----- 289
QY 283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEIEKPDTEI---QAFLLPPVFN 339
Db 290 -----LIYGNFEDKRFV----PAEKIVINFTILNISDDSKISHQMSLLGKSSDV 336
QY 340 RSLSDSFHIYGAPKQSGNTPIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVD 391
Db 337 SSLND-----PQPSGNLRPPQEEVVKHLYGASHLMELIFCDSEENTEGTSFTQESL 388
QY 392 --TVPNLKPLTVY 402

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Db           |:| | : |  
              389 SRIPDKTVIEY 401

Search completed: January 17, 2006, 07:36:14  
Job time : 18.7109 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: January 17, 2006, 07:06:37 ; Search time 23.4755 Seconds  
(without alignments)  
1643.539 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427  
Perfect score: 2141  
Sequence: 1 GKNLKSPQKVEVDIIDNFI.....AHTMDEKLNKSSVPSDAVCE 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	100.0	557	2 A32694	interferon alpha/b
2	1384.5	64.7	560	2 S27387	interferon alpha r
3	966	45.1	590	2 A45283	interferon alpha/b
4	220	10.3	325	2 A47003	cytokine receptor
5	217.5	10.2	349	2 J06311	interferon recepto
6	199	9.3	332	2 A49947	interferon gamma r
7	148	6.9	337	2 I38500	interferon gamma r
8	123.5	5.8	1443	2 I50600	neogenin - chicken
9	123	5.7	1375	2 T13822	frazzled gene prot
10	123	5.7	1526	2 T13823	frazzled gene prot
11	122.5	5.7	1451	2 S42167	190K protein. - hum
12	120	5.6	2057	2 P90109	splicing factor Pr
13	118	5.5	489	2 A31555	interferon gamma r
14	118	5.5	981	2 S11604	receptor-like tyro
15	118	5.5	1005	2 S49015	receptor tyrosine
16	117.5	5.5	1383	2 A36080	insulin receptor p
17	117.5	5.5	1427	2 I51669	tumor suppressor
18	117.5	5.5	1585	2 T19121	probable protein-t
19	117	5.5	817	2 A48721	titin, muscle - ch
20	115.5	5.4	658	2 T16040	hypothetical prote
21	115	5.4	26926	1 I38344	titin, cardiac mus
22	113	5.3	1450	2 A44027	165k myofibrillar
23	113	5.3	1615	2 B49502	protein-tyrosine-p
24	113	5.3	1767	2 A49502	protein-tyrosine-p
25	111.5	5.2	1896	2 T08851	Down syndrome cell
26	111	5.2	6831	2 A88852	protein unc-22 (im
27	111	5.2	6839	2 S27242	twitchin (similar
28	111	5.2	7160	2 T27935	hypothetical prote
29	110.5	5.2	1898	2 S46216	leukocyte antigen-

30 110 5.1 1912 2 A56178 protein-tyrosine-p  
31 109.5 5.1 575 2 A49667 interleukin-10 rec  
32 109.5 5.1 657 2 D81308 probable integral  
33 109 5.1 416 2 T25036 hypothetical prote  
34 108.5 5.1 2215 2 T00348 Lrll protein - mou  
35 108 5.0 991 2 I78843 receptor protein-t  
36 107.5 5.0 1372 2 A34157 insulin receptor p  
37 105.5 4.9 574 2 D81372 probable outer-mem  
38 105.5 4.9 878 1 A40091 interleukin-3 rece  
39 105.5 4.9 1825 2 C88400 protein H19M22.1 f  
40 105.5 4.9 1825 2 T32828 hypothetical prote  
41 105 4.9 56 2 S41602 interferon alpha r  
42 105 4.9 1027 2 B90527 atp-binding protei  
43 104.5 4.9 1447 2 A54100 tumor suppressor p  
44 104 4.9 896 1 A35782 cytokine receptor  
45 104 4.9 1239 1 A32579 neuroglian - fruit

ALIGNMENTS

RESULT 1

A32694  
interferon alpha/beta receptor precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 09-Jul-2004  
C/Accession: A32694; S17112  
R/Uze, G.; Lutfalla, G.; Gresser, I.  
Cell 60, 225-234, 1990  
A/Title: Genetic transfer of a functional human interferon alpha receptor into mouse cell  
A/Reference number: A32694; MUID:90124632; PMID:2153461  
A/Accession: A32694  
A/Molecule type: mRNA  
A/Residues: 1-557 <UZE>  
A/Cross-references: UNIPROT:P17181; UNIPARC:UPI000002D51B; GB:J03171; NID:g184645; PIDN:  
R/Lutfalla, G.  
submitted to the EMBL Data Library, July 1991  
A/Description: The structure of the human interferon alpha/beta receptor gene.  
A/Reference number: S17112  
A/Accession: S17112  
A/Molecule type: DNA  
A/Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>  
A/Cross-references: UNIPARC:UPI0000179801; EMBL:X60459; NID:g32671  
C/Genetics:  
A/Gene: GDB:IFNARI; IFNAR; IFRC  
A/Cross-references: GDB:I20078; OMIM:107450  
A/Map position: 21q22.1-21q22.1  
A/Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3  
C/Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F/1-21/Domain: transmembrane #status predicted <TRN1>  
F/437-455/Domain: transmembrane #status predicted <TRN2>  
F/50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate (As

Query Match	100.0%	Score	2141	DB 2	Length	557	
Best Local Similarity	100.0%	Pred. No.	3.9e-153				
Matches	401	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	GKNLKSPQKVEVDIIDNFI	LRNRSDES	GVGNVTFSPDYQKTGM	DNWIKLSGCQNTSTK	60	
Db	27	GKNLKSPQKVEVDIIDNFI	LRNRSDES	GVGNVTFSPDYQKTGM	DNWIKLSGCQNTSTK	86	
Qy	61	CNFSLLKLVYEEIKLR	IAEKENTSSWY	VDSTFPPRKAQIGP	PEVHLEADKAIVIH	120	
Db	87	CNFSLLKLVYEEIKLR	IAEKENTSSWY	VDSTFPPRKAQIGP	PEVHLEADKAIVIH	146	
Qy	121	SPGTKDSVMWALDGLS	FTSYSLIWKNS	SGVEERIENIYSR	KIYKLSPTTYCLVK	180	
Db	147	SPGTKDSVMWALDGLS	FTSYSLIWKNS	SGVEERIENIYSR	KIYKLSPTTYCLVK	206	
Qy	181	LTSWKIGVYSPVHC	IKTTVENELPP	ENIEVSQNVQNTV	LKWDYTYANNTFO	240	
Db	207	LTSWKIGVYSPVHC	IKTTVENELPP	ENIEVSQNVQNTV	LKWDYTYANNTFO	266	

QY 241 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
QY 301 EIOAFLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYEIFWNTSNAERKIIIE 360  
Db EIOAFLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYEIFWNTSNAERKIIIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 401  
Db KKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 427  
RESULT 2  
S27387  
Interferon alpha receptor type 1 precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S27387; S33770  
R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.  
FEBS Lett. 313, 255-259, 1992  
A;Title: Specific antiviral activities of the human alpha interferons are determined at  
A;Reference number: S27387; MUID:93076908; PMID:1446745  
A;Accession: S27387  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-560 <MOU>  
A;Cross-references: UNIPROT:Q04790; UNIPARC:UPI000012698; EMBL:X68443; NID:g431; PIDN:Q  
A;Experimental source: MDBK cells  
R;Lim, J.K.; Langer, J.A.  
Biochim. Biophys. Acta 1173, 314-319, 1993  
A;Title: Cloning and characterization of a bovine alpha interferon receptor.  
A;Reference number: S33770; MUID:93305725; PMID:8318540  
A;Accession: S33770  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-421, 'V', 423-560 <LIM>  
A;Cross-references: UNIPARC:UPI0000167C2D; EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PI  
A;Experimental source: lung  
A;Keywords: antiviral; cytokine receptor; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <Sig>  
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>  
Query Match 64.7%; Score 1384.5; DB 2; Length 560;  
Best Local Similarity 64.0%; Pred. No. 2.7e-96;  
Matches 258; Conservative 62; Mismatches 78; Indels 5; Gaps 5;  
QY 3 NLKSPQKVEVDIIDDNPFILRNWRSDESVGNVTFSDYQKTMGMNWKLSGCGNITSTKCN 62  
Db NLK-PENVEITHIIDDNPFILRNWRSDESVGNVTFSDYQKTMGMNWKLSGCGNITSTKCN 85  
QY 63 FSSIKL-NVYEEIKLRIRAEK-ENTSSWYVDSTPTPRKAOIGPPEVHLEAEKAIYIHI 120  
Db FSSVELENPEKELIRIRAEENNTSTWYVEVPVPPLEAQIGPPDVHLEAEKAILIIS 145  
QY 121 S-PGTGDSVNMWALDGLSFTYSLIWNKSSGVBERIENYSRHKIYKLSPETTYCLKVKAA 179  
Db SSGVLEENPEKELIRIRAEENNTSTWYVEVPVPPLEAQIGPPDVHLEAEKAILIIS 145  
QY 146 SPGTGDSINWANDRSFRSVVIWNKSSLSLEERTETVYPEDKIYKLSPIITTYCLKVKAZ 205  
Db LRLQSRVGCYSPVVCINTTHERHKVSPDENIQINADNQIYVLKWDYPYENATFQAQWLRAF 265  
QY 180 LLTSWKIGVYSPVHCIKTKTYVENLPPPTENIEVSQVQNYVYLKWDYTYANNMTFQVQMLHAF 239  
Db LLTSWKIGVYSPVHCIKTKTYVENLPPPTENIEVSQVQNYVYLKWDYTYANNMTFQVQMLHAF 239  
QY 206 LRLQSRVGCYSPVVCINTTHERHKVSPDENIQINADNQIYVLKWDYPYENATFQAQWLRAF 265  
Db LRLQSRVGCYSPVVCINTTHERHKVSPDENIQINADNQIYVLKWDYPYENATFQAQWLRAF 265  
QY 240 LKRNPGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 299  
Db LKRNPGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
QY 266 FKXIPGNHSDKWKQIPDCENVTSTHCVFPPEVSRGIVYVRASNGNGTSFWSSEIKFBN 358  
Db FKXIPGNHSDKWKQIPDCENVTSTHCVFPPEVSRGIVYVRASNGNGTSFWSSEIKFBN 385  
QY 300 TEIOAFLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYEIFWNTSNAERKIIIE 360  
Db TEIOAFLPPVFNIRSLSDSHYIYGAPKQSGNTPIQDYPLIYEIFWNTSNAERKIIIE 386  
QY 326 TENKTIIFPPIVSKSVTSDSLHVSVCASESESNVQYPLIYEIFWNTSNAERKIIIE 360  
Db TENKTIIFPPIVSKSVTSDSLHVSVCASESESNVQYPLIYEIFWNTSNAERKIIIE 386  
QY 359 IEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 401  
Db IEKKTDTVTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSFSDAVCE 427

Db 386 LEKRTNFIFPDLKPLTVYCVKARALIENDRRNKGSSFSFSDTVC 428  
RESULT 3  
A45283  
Interferon alpha/beta receptor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 25-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429  
R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudmon, D.; Mogensen, K.E.  
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992  
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp  
A;Reference number: A45283; MUID:92262522; PMID:1533935  
A;Accession: A45283  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-590 <UZE>  
A;Cross-references: UNIPROT:P33896; UNIPARC:UPI0000027A2F; GB:M89641; NID:g194111; PIDN:A  
A;Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIP:102357)  
R;Lutfalla, G.; Uze, G.  
Gene 148, 343-346, 1994  
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq  
A;Reference number: I48423; MUID:95047447; PMID:7958966  
A;Accession: I48423  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 118-125 <RES>  
A;Cross-references: UNIPARC:UPI0000000524; EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PI  
A;Accession: I48424  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 127-224 <RES2>  
A;Cross-references: UNIPARC:UPI0000000525; EMBL:U06238; NID:g497104; PIDN:AAAC01749.1; PI  
A;Accession: I48425  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 243-264 <RES3>  
A;Cross-references: UNIPARC:UPI0000000526; EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PI  
A;Accession: I48426  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 265-375 <RES4>  
A;Cross-references: UNIPARC:UPI0000000527; EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PI  
A;Accession: I48427  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 397-424 <RES5>  
A;Cross-references: UNIPARC:UPI0000000528; EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PI  
A;Accession: I48428  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 426-445 <RES6>  
A;Cross-references: UNIPARC:UPI0000000529; EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PI  
A;Accession: I48429  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 473-590 <RES7>  
A;Cross-references: UNIPARC:UPI000000052A; EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PI  
C;Genetics:  
A;Gene: IFNAR  
A;Introns: 177/3; 331/1  
C;Keywords: cytokine receptor; transmembrane protein  
Query Match 45.1%; Score 966; DB 2; Length 590;  
Best Local Similarity 47.8%; Pred. No. 8.3e-65;  
Matches 192; Conservative 71; Mismatches 130; Indels 10; Gaps 4;  
QY 1 GNKLSPQKVEVDIIDDNPFILRNWRSDESVGNVTFSDYQKTMGMNWKLSGCGNITSTK 60  
Db GNKLSPQKVEVDIIDDNPFILRNWRSDESVGNVTFSDYQKTMGMNWKLSGCGNITSTK 85  
QY 61 CNPSSLKNVYEEIKLRIRAEKEN-TSSWYVDSFTTFRKAOIGPPEVHLEAEKAIYIHI 119  
Db CNPSSLKNVYEEIKLRIRAEKEN-TSSWYVDSFTTFRKAOIGPPEVHLEAEKAIYIHI 119

Db 86 CEPILLDTNVYIKQFRVRAEGNSTSSWNEVDPIPFYTAHMSPPVRLAEADKAILVH 145

Qy 120 ISPTKDSVMWALDGLSFTYSLLLWKNSGSGVEERIENIYSRHKYIKLSPETTYCLVKVAA 179

Db 146 ISPPQDGNMWALEKPSFSYIRIWQKSSDKTINSTYYVEKIPPELLPETTYCLEVKAI 205

Qy 180 LLTSKIGVSPVHCITKTVENELPPENIEVSQONQYVLKWDY-TYANMTFQVOMLHA 238

Db 206 HPSLKSHNSTVQCISTTVANKMPVGNLQVDAQSKSYVLKWDYIASADVLFRQWLPG 265

Qy 239 FLKKNPGNHLKQIIPDCENKVTQCVFPQNVQKGIYLLRVOAGDNNTSFSWEIKF 298

Db 266 YSKSSGSHSDKWPICPCANQVTHCVFSQDTYVTGTFLLVQASGNHTSFSWEKFI 325

Qy 299 DTEOAFLLPPVFNIRSLSDSFHYIYGAPKOSGNTPVQDYPLIYEIFWENTSNAERKI 358

Db 326 DSQKHILPPPPVITVTAMSDTLVVVNCQDSTCD-----GLNVEIIFWENTSNTKISM 378

Qy 359 IEKTDVTVPNLKLTIVYCVKARHTWDEKLNKSVSFSDAVCE 401

Db 379 EKDGPFEFTLNLOPLTVYCVQARV-LFRALLNKTSNFSEKLCE 420

RESULT 4

A47003

cytokine receptor family class II protein CRF2-4 precursor - human

C:Species: Homo sapiens (man)

C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004

C:Accession: A47003; G01418

R:Lutfalla, G.; Gardiner, K.; Uze, G.

Genomics 16, 366-373, 1993

A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less

A:Reference number: A47003; MUID:93300510; PMID:8314576

A:Accession: A47003

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-325 <LUT>

A:Cross-references: UNIPROT:Q08334; UNIPARC:UPI0000048F14; GB:Z17227; NID:G393378; PIDN: submitted to the EMBL Data Library, April 1994

A:Reference number: G06935

A:Accession: G01418

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-123, 'D', 125-268, 'VGRME' <LUT>

A:Cross-references: UNIPARC:UPI000016A09D; EMBL:U08988; NID:G571295; PID:G571296

C:Genetics:

A:Gene: GDB:CRFB4; CRF2-4

A:Cross-references: GDB:138168; OMIM:123889

A:Map position: 21q; 21q22.1-21q22.2

A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1

C:Keywords: transmembrane protein

Query Match 10.3%; Score 220; DB 2; Length 325;

Best Local Similarity 30.0%; Pred. No. 4.2e-09;

Matches 61; Conservative 41; Mismatches 89; Indels 12; Gaps 7;

Qy 7 POKVEVDIIDNFILRNRSDESIGNVTFSFDYQKTMGNWIKLSGCONITSTKCNFSSL 66

Db 24 PENVRMNSVFNKILQWESPAFAGNLFTTAQY----LSYRIFQDKCMNTLTTECDRSS- 78

Qy 67 KLVNVEEIKLRIRAE-KENTSSWYEVDSFTFPRKQIGPPEVHLEA-EDKAIIVHISPT 124

Db 79 -LSKYGDHTLRVRAEFADEHSDWNI-TFCVPVDDTIIGPGMGVQVEVLADSLMRFLAPKI 136

Qy 125 KDSV-MWALDGL--SFTYSLLLWKNSGSGVEERIENIYSRHKYIKLSPETTYCLVKVAKALL 181

Db 137 ENYETVTMKVYNSTVNVQWKNGTDEKQITPDYDFEVLRLNLEPWTTCVQVRGFLP 196

Qy 182 TSWKIGVSPVHCITKTVENELP 204

Db 197 DRNKGWSEPVCEGTHDEIVP 219

RESULT 5

JC6311

interferon receptor-class II cytokine receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C:Accession: JC6311

R:Gibbs, V.C.; Pennica, D.

Gene 186, 97-101, 1997

A:Title: CRF2-4: isolation of cDNA clones encoding the human and mouse proteins.

A:Reference number: JC6311; MUID:97199375; PMID:9047351

A:Accession: JC6311

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-349 <GIB>

A:Cross-references: UNIPROT:Q8VHM7; UNIPARC:UPI000017C6DE; GB:U53696

Query Match 10.2%; Score 217.5; DB 2; Length 349;

Best Local Similarity 28.4%; Pred. No. 7.1e-09;

Matches 60; Conservative 45; Mismatches 79; Indels 27; Gaps 9;

Qy 7 POKVEVDIIDNFILRNRSDESIGNVTFSFDYQ-KTGMNWKLSGCONITSTKCNFS 64

Db 24 PEKVRMNSVFNKILQWEPAPKTNLTFTAQYSYRSFQDH-----CKRTASTQCDPS 77

Qy 65 SLKLVNVEEIKLRIRAE-KENTSSWYEVDSFTFPRKQIGPPEVHLEADKAIIVHIS-- 121

Db 78 --HLSKYGDYTVRRAELADEHSEWNV-TCPVEDTIIGPPEMQIESLAESLELRFSA 134

Qy 122 -----PGTKDSVMWALDGL--SFTYSLLLWKNSGSGVEERIENIYSRHKYIKLSPETTYCL 174

Db 135 QIENEPEP-----WTLKNIYDSWAYRVQYQWKNRKFQVVSYPYDSEVLRLNLEPWTTCI 189

Qy 175 KVKAALLTSMKIGVYSPVHCITKTVENELPP 205

Db 190 QVQGFLLDQNKRTGEWSBPIC-ERTGNDEITP 219

RESULT 6

A49947

interferon gamma receptor beta subunit - mouse

N:Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor; type I

C:Species: Mus musculus (house mouse)

C>Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A49947

R:Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.

Cell 76, 803-810, 1994

A:Title: A novel member of the interferon receptor family complements functionality of t

A:Reference number: A49947; MUID:94170381; PMID:8124717

A:Accession: A49947

A:Molecule type: mRNA

A:Residues: 1-332 <HEM>

A:Cross-references: UNIPROT:Q63953; UNIPARC:UPI0000022068; GB:S69336; NID:G545841; PIDN:

A:Experimental source: early B-cell line Y16

A>Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)

C:Keywords: cytokine receptor

Query Match 9.3%; Score 199; DB 2; Length 332;

Best Local Similarity 30.1%; Pred. No. 1.6e-07;

Matches 65; Conservative 38; Mismatches 81; Indels 32; Gaps 12;

Qy 4 LKSPQKVEVDIIDNFILRNRSDES-----VGNVTFSFDYQKTMGNWIKL--SGCQ 54

Db 29 LAAPLNPRHLNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSHRLLPEPNT 82

Qy 55 NITSTKCNFSS---LKLNVYE-EIKLRIRAKEN-TSSWYEVDSFTFPRKQIGPPE-VH 108

Db 83 DITETKCDLTGGKRLKLPHPFTFLRVRAKGNLTSKWVGLEPFQHYENVTVGPKNIS 142

Qy 109 LEAEDKAIIVHISPTKDSVMWALDGLSFTYSLLLWKNSGSGVEERIENIYSRHKYI--KL 166

Db 143 VTPGKGLVIHFSPFD-----VFHGATFQYLHVWSEKSEQQVEGPFKSNISVLGNL 197

Qy 167 SPETTYCLVKAAL-LTSWKI---GVYSPVHCIKTT 198  
| | | | | : | | | | : | | | | : | |  
Db 198 KPRVYVCLQTEAQLKLNKKIRPHGLLSNVSCHETT 233

RESULT 7  
138500  
interferon gamma receptor accessory factor-1 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: I38500; I38501  
R:Sch, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.  
Cell 76, 793-802, 1994  
A:Title: Identification and sequence of an accessory factor required for activation of b  
A:Reference number: A49946; MUID:94170380; PMID:8124716  
A:Accession: I38500  
A:Molecule type: mRNA  
A:Residues: 1-337 <RES>  
A:Cross-references: UNIPROT:P38484; UNIPARC:UPI000012D65E; EMBL:U05875; NID:G463549; PID  
A:Experimental source: clone pSK1  
A:Accession: I38501  
A:Molecule type: mRNA  
A:Residues: 1-63, Q', 65-337 <RE2>  
A:Cross-references: UNIPARC:UPI00001514B0; EMBL:U05877; NID:G463551; PIDN:AAA16956.1; PT  
A:Experimental source: clone pJS3  
C:Genetics:  
A:Map position: 21  
C:Keywords: cytokine receptor

Query Match 6.9%; Score 148; DB 2; Length 337;  
Best Local Similarity 22.2%; Pred. No. 0.0011;  
Matches 62; Conservative 49; Mismatches 104; Indels 64; Gaps 13;

Qy 4 LKSPQKEVDIIDDNFILRW-----NRSDSGVNTFTFDYQKTGMWNWIKLS----- 51  
Db 30 LPAPQHPKIRLYNAEQVLSPEVALSNSTRPVYRVQFKYTDSK-----WFTADIMSIGV 84

Qy 52 GQCNITSTKCNFSS-----LKLNVYEEIKLIRAEKENT-SSWYEVDSFTPFKRAQI 102  
| | | | | : | | | | : | | | | : | |  
Db 85 NCTQITATEDCFIAASPSAGFMDFNV-----TLRLAELGALHSAWTMTFQHYRNVTV 140

Qy 103 GPPEVHLE---AEDKAIVIHISPTKDSVMWALDGLSFTYSLLIWNSSGVSEERIENIYS 159  
| | | | | : | | | | : | | | | : | |  
Db 141 GPPE-NIEVTPGEGSLIIRFSSPDIA DTSTAP---FCYVHYWE--KGIQVQVKGPPR 193

Qy 160 RHKIY--KLSPETTYCLVKAALTS-----WKIGVYSPVHCIKTTVENELPPENIEVS 213  
| | | | | : | | | | : | | | | : | |  
Db 194 SNSISLNLKPSRYVCLQVQAQLLWKNKSNIFRVGHLNISISETMADASTELQOVILISV 253

Qy 214 -----QNNYVLKWDYTVANNMTFOVQ 234  
Db 254 GTPSLLSVLAGCFVLKRGILKYWHFTPPSIPLQIE 292

RESULT 8  
150600  
neogenin - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50600  
R:Vielmetter, J.; Kayyem, J.F.; Roman, J.M.; Dreyer, W.J.  
J. Cell Biol. 127, 2009-2020, 1994  
A:Title: Neogenin, an avian cell surface protein expressed during terminal neuronal diff  
A:Reference number: A55193; MUID:95105243; PMID:7806578  
A:Accession: I50600  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1443 <VIE>  
A:Cross-references: UNIPROT:Q90610; UNIPARC:UPI0000012F2F; EMBL:U07644; NID:G641965; PID

Query Match 5.8%; Score 123.5; DB 2; Length 1443;  
Best Local Similarity 22.0%; Pred. No. 0.57;

Matches 89; Conservative 60; Mismatches 194; Indels 61; Gaps 19;  
Qy 6 SPQKEVDIIDDNFILRWNR---SDSGVNTFTFDYQKTGMWNWIKLSGCONITSTKCN 62  
| | | | | : | | | | : | | | | : | |  
Db 427 APRDVATLVSTRFIRLTWRTFVSDPQGDNLTYISFTYKEG-----INRIVEN-TSRPGE 481

Qy 63 FSSLKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKRAQIGPPEVHLEAEDKAIVIHISP 122  
| | | | | : | | | | : | | | | : | |  
Db 482 TQVMIQNLMPETVYVFRVVAQNKHGHE--SSAPLKVAT--QPEVQLPGPAPNIRAYAGS 537

Qy 123 GTKDSVMWAL-----DGLSFTYSLLIWNSSGVSEERIENIYSRHKIYKLSPETTYCLVKA 178  
| | | | | : | | | | : | | | | : | |  
Db 538 PTVTWTETPLSGNGEIQNYKLYMEKQDSQDQDVAGLSYTTITGLKKYTESFRVA 597

Qy 179 ALLTSWKIGVYSPVHCIKTTVENELPPENIEVSQN-QNYVLKWDYTVANNMTFOVQWLH 237  
| | | | | : | | | | : | | | | : | |  
Db 598 --YKNGPGVSTQDVVVRTLSVPSAAPQNLTEARNRSKSIIMLHWQPPPA----- 645

Qy 238 AFLKRNPGNHL-----YKWKQIPDCENVKTCQVFPQNVFQ--KGI-----YLLRVOASD 285  
| | | | | : | | | | : | | | | : | |  
Db 646 -----GTHSGQITGKIRYKVRKSDVTSVGGTQLFLIEGLERGTEYNFRIAAMT 698

Qy 286 GNNVT---SFWSEBIKFDTEIQAFLLPPV---FNIRSLSDSFHYIYGAPKOSGNTPVIQDY 339  
| | | | | : | | | | : | | | | : | |  
Db 699 VNGTGPATQWVSATFESDLDSKRVPEVPSLSLHVRPLVTSI-VVSWTTPPENQNI-VVRGY 756

Qy 340 PLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA 382  
| | | | | : | | | | : | | | | : | |  
Db 757 AIGYGI-----GSPAQTIKVDYKQRYTYIENLDPSSHYVITLKA 796

RESULT 9  
T13822  
frazzled gene protein - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13822  
R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, Y.  
Cell 87, 197-204, 1996  
A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is  
A:Reference number: Z17780; MUID:97015076; PMID:8861904  
A:Accession: T13822  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1375 <KOI>  
A:Cross-references: UNIPROT:Q94537; UNIPARC:UPI00000422DD; EMBL:U71001; NID:G1621114; PID  
C:Genetics:  
A:Gene: frazzled  
A:Cross-references: FlyBase:FBgn0011592  
A:Map position: 2  
C:Function:  
A:Description: may function in vivo as a receptor or component of a receptor mediating Ne

Query Match 5.7%; Score 123; DB 2; Length 1375;  
Best Local Similarity 16.3%; Pred. No. 0.58;  
Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;

Qy 1 GKWLKS-----PQKEVDIIDDNFILRW-----NRSDSVG 31  
| | | | | : | | | | : | | | | : | |  
Db 448 GKPLDSGLQARLPSPQRDLVAQIVKSRFVTLSSWVEPLQAGDVVYTVYVYKMNSSEREQK 507

Qy 32 NVTFSFDYQKTGMWNWIKLSGCONITSTKCNFSS-----LKLNVYEEIKLR----- 77  
| | | | | : | | | | : | | | | : | |  
Db 508 MVTKSHDDQOVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTOPEVNIAGPPRNFE 567

Qy 78 -IRAEKENTSSWYE-----PPEVHLE-AEDKAIVIHISPTKDSVMWALD 92  
| | | | | : | | | | : | | | | : | |  
Db 568 YARSHKEIYVKNWEEPTVTNGEILKYRVYSENDSGLADYHSDTALEAVLTALPHTDYVI 627

Qy 93 SFTPFKRAQIG-----PPEVHLE-AEDKAIVIHISPTKDSVMWALD 133  
| | | | | : | | | | : | | | | : | |  
Db 628 SVVFFNRNGMGDSABIRVKFTSSTPSPNNVTLEVTSSSITVHWEPABEDRNGQIT 687



Qy 134 GLSTYLLIWNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAALL-----TSWKIG 187  
Db 688 GYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTWNR 744  
Qy 188 VYSPVHCIKTTVENELP-----PPENIEVSQVONQYVLKW 222  
Db 745 -----NTLENDLDETQVPGKPIWISHPGANNIALHWGPPQHPEIKI--RNYVLGW 793  
Qy 223 -----DY-----  
Db 794 GRGIPDENTIELKETERYHILKNLESNMDYVVSRLARNVKGDPPIYDNIKTRDEEPVDA 853  
Qy 225 -----TYANMTFOVQWLHAFLEKRN-----PGNHLYKWKQIPD 256  
Db 854 PTPLEVPVGLRAITMSSSIIVVYIDTMLNKNQHVTDNHRHYTVSYGITGSNRURY-- 908  
Qy 257 CENVKTTQCVPQNVFQKGIYLLRQVADSGNNTSFWESEIKFDEIQAFLLPPVFNIRSL 316  
Db 909 -HNTTDLNLCMI-NDLRNTQYEFAPVVKVGRRESSWSVLNSTYQNVPTVTPP----- 959  
Qy 317 SDSPHIYGAPKQSGNTPVIOQYP-----LIYEIIFWENTISNAER-----KIIBKKT 363  
Db 960 ---REVTVRLDEMNPPTVIVQWIPPKHTLGOITGYNIIYTTDTTKRDRDSVEAFAGEET 1016  
Qy 364 DVTVPNLKPLTYVCVKARAHT 384  
Db 1017 MLMLPNLKPYTTYVFKVQART 1037

RESULT 10  
T13823  
Frazzled gene protein, log isoform - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13823  
R:Kolodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, C.S.; Fried, S.; Jan, L.Y.; Jan, Y.  
Cell 87, 197-204, 1996  
A:Title: Frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is  
A:Reference number: 217780; MUID:97015076; PMID:8861904  
A:Accession: T13823  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1526 <COL>  
A:Cross-references: UNIPROT:Q94538; UNIPARC:UPI000007A6FA; EMBL:U71002; NID:g1621116; PI  
C:Genetics:  
A:Gene: frazzled  
A:Cross-references: FlyBase:FBgn0011592  
A:Map position: 2

Query Match 5.7%; Score 123; DB 2; Length 1526;  
Best Local Similarity 16.3%; Pred. No. 0.67;  
Matches 101; Conservative 68; Mismatches 184; Indels 268; Gaps 22;  
Qy 1 GKNLKS-----PKQVVEDIIDNFI-LRW-----NRSDESVG 31  
Db 599 GKPLDSGLQARLPSPQRLVAQIVKSRFVTLWSVEPLQAGDVVYTVYVYKMNNSEREQK 658  
Qy 32 NVTFSFDYQKTMNDWIKLSCQNTITSTKCNFSS-----LKLNVYBEIKL----- 77  
Db 659 MVTKSHDDQVNIQSLPRTYQFRVEANTFNGSGASSAPLEVSQPEVNIAGPPRNFEG 718  
Qy 78 -IRAEKENTSSWY-----  
Db 719 YARSHKEIYVWKEEPTVTNGEILKYRVYSENDSADLYHDSTALEAVLTLPHTDVI 778  
Qy 93 SFTPPRKAQIG-----PPEVHLE-AEDKAIVIHISPGTKDSVNMALD 133  
Db 779 SVVPPNRNGMDSSAEIRVKTFSSTPSPNNVTLEVTSSSIIVHWEPPAEEDRNGQIT 838  
Qy 134 GLSFTYLLIWNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAALL-----TSWKIG 187  
Db 839 GYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTWNR 895

Qy 188 VYSPVHCIKTTVENELP-----PPENIEVSQVONQYVLKW 222  
Db 896 -----NTLENDLDETQVPGKPIWISHPGANNIALHWGPPQHPEIKI--RNYVLGW 944  
Qy 223 -----DY-----  
Db 945 GRGIPDENTIELKETERYHILKNLESNMDYVVSRLARNVKGDPPIYDNIKTRDEEPVDA 1004  
Qy 225 -----TYANMTFOVQWLHAFLEKRN-----PGNHLYKWKQIPD 256  
Db 1005 PTPLEVPVGLRAITMSSSIIVVYIDTMLNKNQHVTDNHRHYTVSYGITGSNRURY-- 1059  
Qy 257 CENVKTTQCVPQNVFQKGIYLLRQVADSGNNTSFWESEIKFDEIQAFLLPPVFNIRSL 316  
Db 1060 -HNTTDLNLCMI-NDLRNTQYEFAPVVKVGRRESSWSVLNSTYQNVPTVTPP----- 1110  
Qy 317 SDSPHIYGAPKQSGNTPVIOQYP-----LIYEIIFWENTISNAER-----KIIBKKT 363  
Db 1111 ---REVTVRLDEMNPPTVIVQWIPPKHTLGOITGYNIIYTTDTTKRDRDSVEAFAGEET 1167  
Qy 364 DVTVPNLKPLTYVCVKARAHT 384  
Db 1168 MLMLPNLKPYTTYVFKVQART 1188

RESULT 11  
S42167  
190K protein - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S42167  
R:Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O.  
J. Cell Sci. 106, 319-330, 1993  
A:Title: The globular head domain of titin extends into the center of the sarcomeric M  
A:Reference number: S42166; MUID:94095665; PMID:7505783  
A:Accession: S42167  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1451 <VIN>  
A:Cross-references: UNIPROT:P52179; UNIPARC:UPI000012FB8B; EMBL:X69090; NID:g407098; PID  
C:Superfamily: skelemin

Query Match 5.7%; Score 122.5; DB 2; Length 1451;  
Best Local Similarity 19.8%; Pred. No. 0.68;  
Matches 91; Conservative 66; Mismatches 181; Indels 121; Gaps 21;  
Qy 17 DNFTLRNRSDESVDGN--VTFSPDYQKTMNDWIKLSCQNTITSTKCNFSSLKLNVYEEI 74  
Db 388 DYIIISWKPQAVDGGSPILGFIKCEVGTDSW-----SQCNMTVPKFAFPVPT 436  
Qy 75 KL-----RIRAEKENTSSW-----YEVDSTFPFRKAQIGPPEVHLEAEDKAIVIHIS 121  
Db 437 GLIEGRSYIFRVRVAVNKGIGFPPSRVSEAVAAALDPAEKARLKSP---LSTLDWTIVITEE 493  
Qy 122 PGTKDSVNMALDGLSFT-----YSLLIWK-----NSGVEERIENIYS----- 159  
Db 494 EPSEGIYVGPPTDLSVTEATRSYVVLWSKPGQRGHEGIMYFVEKCEAGTENWQVNTTEL 553  
Qy 160 -----RHKIYKLSPTTYCLKVKAALLTSWKIGIYVSPVHCIKTTV-----ENELP 204  
Db 554 PVKSPRFLPDLAEKGYCYCFVRVC-----SNSAGVGESEATEVTVVGVGDKLDIPKAPGKII 609  
Qy 205 PPENIEVSQVONQYVLKW-----YYANMTFOVQWLHAFLEKRN--GNHLYKWK 252  
Db 610 PSRNTDTSV-----VSWSEESKADKELGVYIEANVAGSGKWEPC--NNNPVKTHRP--- 659  
Qy 253 QIPDCENVKTTQCVPQNVFQKGIYLLRQVADSGNNTSFWESEIKFDEIQAFLLPP--- 309  
Db 660 ---TCHGLVTQS-----YIFRVRVAVNAGLSEYSQDSE-AIEVKAATAPPSP 704  
Qy 310 ---VFNIRSLSDSFHYIYKAPQSGNTPVIOQYPLIYEI-----FWENTSNAERKIEBK 362  
Db 705 CDITCLSFSDSMVLGKQPKDGTGAETGYVYVYREVIGDVGPGKWR---BANVKAVERE 761



```
Qy 162 KIYKLSPTTYCLVKVKAALLTSWIKGVYSPVH-----CIKTTVENELPP----- 205
Db 310 GFFKASPHSQTCSCKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTWACTRP 359
Qy 206 ---PENIEVSQONQNYVLKW-----DYTYANMTFFQVQWLHAFILKRNPGNHLKWK 252
Db 360 PSAPRNALSNVNETSVFLEWIPPADTGGGKDVSYIILCKKN-SHAGVCECGGHR--- 415
Qy 253 QIPDCENVKTTQCVPFQNGIYLLRVQASDGNNTSFWESEIKFDTEIOAFLLPPVFN 312
Db 416 -----YLPQOIGLKNTSVMMADPLAHTNYTF-----EIEA-----VNG 448
Qy 313 IRSLSDSFHHIYG---APKQSGNTPVIQ-----DYP-----LIYEIIF 347
Db 449 VSDLSPGTRQYVSNNVTNQAAPSPVTVNKKIAKNSISLSWQEPDRPNNGIILEYEIKY 508
Qy 348 WENTSNAERKLIIE-KKTDVTVPNLKLTVYCVKARAHT 384
Db 509 FEKQDQTSYTIKSKETTITAEGLKPASVYVFOIRART 546
```

## RESULT 15

```
S49015
receptor tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S49015; S51602
R:Maisonnier, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777; PMID:7504232
A:Accession: S49015
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1005 <MAI>
A:Cross-references: UNIPROT:P54757; UNIPARC:UPI00000508E8; EMBL:S68024
A:Note: the authors translated the codon GAC for residue 170 as Glu
A:Accession: S51602
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305, 'G', 359-1005 <MA2>
A:Cross-references: UNIPARC:UPI0000175665; EMBL:S68026
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:675-941/Domain: protein kinase homology <KIN>
F:683-691/Region: protein kinase ATP-binding motif
```

```
Query Match 5.5%; Score 118; DB 2; Length 1005;
Best Local Similarity 20.1%; Pred. No. 0.9;
Matches 92; Conservative 51; Mismatches 165; Indels 150; Gaps 21;

Qy 1 GKNLKSPQKVEVDII--DDNF-----ILRNRSDESIGNVT---FSFDYQKTMGNW 47
Db 165 GRNIKDNQYIKIDTIAADESEFELDLGRVMKLTVEVRDVGPLSKKGFYLAQDVG---- 220
Qy 48 IKLSGQNITST-----KCNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQI 102
Db 221 ----ACIALSVRVYKKCPSVVRHLAVFPD-----TTGADSSQLLEVSGSCVNHSTVD 271
Qy 103 GPPEVHLBAEDKAIIVIHISPGTKDSVMWALDGLSFTSYLLIWNKSSGVVEERIENI-YSRH 161
Db 272 DPPKWHCSAEGELV---PIGKMC-----KAGYEKNGTCQVCRP 309
Qy 162 KIYKLSPTTYCLVKVKAALLTSWIKGVYSPVH-----CIKTTVENELPP----- 205
Db 310 GFFKASPHSQTCSCKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTWACTRP 359
Qy 206 ---PENIEVSQONQNYVLKW-----DYTYANMTFFQVQWLHAFILKRNPGNHLKWK 252
Db 360 PSAPRNALSNVNETSVFLEWIPPADTGGGKDVSYIILCKKN-SHAGVCECGGHR--- 415
```

```
Qy 253 QIPDCENVKTTQCVPFQNGIYLLRVQASDGNNTSFWESEIKFDTEIOAFLLPPVFN 312
Db 416 -----YLPQOIGLKNTSVMMADPLAHTNYTF-----EIEA-----VNG 448
Qy 313 IRSLSDSFHHIYG---APKQSGNTPVIQ-----DYP-----LIYEIIF 347
Db 449 VSDLSPGTRQYVSNNVTNQAAPSPVTVNKKIAKNSISLSWQEPDRPNNGIILEYEIKY 508
Qy 348 WENTSNAERKLIIE-KKTDVTVPNLKLTVYCVKARAHT 384
Db 509 FEKQDQTSYTIKSKETTITAEGLKPASVYVFOIRART 546
```

Search completed: January 17, 2006, 07:19:44  
Job time : 25.4755 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 06:26:20 ; Search time 79 Seconds  
(without alignments)

2230.264 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427

Perfect score: 2141

Sequence: 1 GKNLSPQKVEVDIIDNFI.....AHTMDKLNKSVFSDAVCE 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A\_Geneseq\_21.\*
- 1: Geneseqp1980s.\*
  - 2: Geneseqp1990s.\*
  - 3: Geneseqp2000s.\*
  - 4: Geneseqp2001s.\*
  - 5: Geneseqp2002s.\*
  - 6: Geneseqp2003as.\*
  - 7: Geneseqp2003bs.\*
  - 8: Geneseqp2004s.\*
  - 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	436	2 AAR14487	Aar14487 Soluble i
2	2141	100.0	436	2 AAR28495	Aar28495 Sequence
3	2141	100.0	436	6 ABU05090	Abu05090 Human exp
4	2141	100.0	436	6 ABU05092	Abu05092 Human exp
5	2141	100.0	436	6 ABU05098	Abu05098 Human exp
6	2141	100.0	557	2 AAR14488	Aar14488 Complete
7	2141	100.0	557	2 AAR11958	Aar11958 Human alp
8	2141	100.0	557	2 AAR28496	Aar28496 Sequence
9	2141	100.0	557	2 AAR42635	Aar42635 Human int
10	2141	100.0	557	6 ABU05091	Abu05091 Human exp
11	2141	100.0	557	6 ABU05095	Abu05095 Human exp
12	2141	100.0	557	6 ABU05094	Abu05094 Human exp
13	2141	100.0	557	6 ABU05107	Abu05107 Human exp
14	2141	100.0	557	6 ABU05099	Abu05099 Human exp
15	2141	100.0	557	6 ABU05106	Abu05106 Human exp
16	2141	100.0	557	6 ABU05097	Abu05097 Human exp
17	2141	100.0	557	6 ABU05093	Abu05093 Human exp
18	2141	100.0	557	6 ABU05100	Abu05100 Human exp
19	2141	100.0	575	8 ADR66319	Adr66319 Human pro
20	2141	100.0	575	8 ADR66661	Adr66661 Human pro
21	2138	99.9	441	9 ADV25067	Adv25067 INR1_T11
22	2137	99.8	557	2 AAR75356	Aar75356 Human IFN
23	2137	99.8	557	6 ABU05102	Abu05102 Human exp
24	2136	99.8	434	2 AAW21805	Aaw21805 Spliced-d

25	2136	99.8	434	6 ABU05104	Abu05104 Human exp
26	2136	99.8	557	2 AAW21804	Aaw21804 Transmembr
27	2136	99.8	557	6 ABU05103	Abu05103 Human exp
28	2136	99.8	575	3 AAB57094	Aab57094 Human pro
29	2136	99.8	575	4 AAB517294	Abg17294 Novel hum
30	2136	99.8	575	6 ABU05096	Abu05096 Human exp
31	2132	99.6	436	2 AAR71723	Aar71723 IFN recepr
32	2132	99.6	436	6 ABU05101	Abu05101 Human exp
33	2124	99.2	631	8 ADK23579	Adk23579 Human IFN
34	2084	97.3	496	2 AAW21806	Aaw21806 Spliced-d
35	2084	97.3	496	6 ABU05105	Abu05105 Human exp
36	1559.5	72.8	458	8 ADH22370	Adh22370 Human rec
37	798	37.3	187	8 ADH22369	Adh22369 Human rec
38	228	10.6	273	6 ABR38950	AbR38950 Human AK1
39	226	10.6	273	6 ABR38949	AbR38949 Human AK1
40	225	10.5	220	5 AAU76911	Aau76911 Human cvt
41	225	10.5	220	8 ADS31753	AdS31753 Human CRF
42	225	10.5	220	8 ADS92755	AdS92753 Human CRF
43	225	10.5	273	6 ABR38944	AbR38944 Human AK1
44	225	10.5	476	5 AAU76912	Aau76912 Human CRF
45	225	10.5	476	6 AAE30845	Aae30845 Human CRF

## ALIGNMENTS

RESULT 1  
AAR14487  
ID AAR14487 standard; protein; 436 AA.  
XX AAR14487;  
AC AAR14487;  
XX  
DT 16-JAN-1992 (first entry)  
XX  
DE Soluble interferon-alpha/beta receptor.  
XX  
KW IFN; autoimmune disease; graft rejection; histocompatibility.  
XX  
OS Homo sapiens.  
XX  
XX  
XX PR2657881-A.  
XX  
XX 09-AUG-1991.  
XX  
XX 05-FEB-1990; 90FR-00001298.  
XX  
XX 05-FEB-1990; 90FR-00001298.  
XX  
XX (EUBI-) LAB EURO BIOTECHNO.  
XX  
XX Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey MG;  
XX Uze G;  
XX  
XX WPI; 1991-319778/44.  
XX N-PSDB; AAQ14239.  
XX  
XX New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
XX used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
XX anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
XX  
XX Claim 2; Page 45; 52pp; French.  
XX  
XX The transmembrane and cytoplasmic domains of the native IFN receptor have  
XX been deleted to obtain a soluble, circulating form of the receptor.  
XX Potentially immunogenic epitopes have thus been eliminated. Derivatives  
XX obtained by substitution or deletion of this sequence are also claimed as  
XX are hybrid molecules comprising the soluble receptor (or deriv.) and an  
XX immunoglobulin such as IgG1. See also AAQ14240  
XX  
XX Sequence 436 AA;  
XX  
XX Query Match 100.0%; Score 2141; DB 2; Length 436;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e-184;

```
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSCQNITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSCQNITSTK 86
QY 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 120
DB 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 146
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLVKVKAAL 180
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLVKVKAAL 206
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLRVQASDGNNTSFWSSEIKFDT 240
DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLRVQASDGNNTSFWSSEIKFDT 266
QY 241 KRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300
DB 267 KRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326
QY 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYETIIFWENTSNAERKIIIE 360
DB 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYETIIFWENTSNAERKIIIE 386
QY 361 KKTDTVTVPNLKPLTYCYVKARAHMTDEKLNKSSVFSDAVCE 401
DB 387 KKTDTVTVPNLKPLTYCYVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 2
AAR28495
ID AAR28495 standard; protein; 436 AA.
AC AAR28495;
XX
XX
DT 25-MAR-2003 (revised)
DT 31-MAR-1993 (first entry)
DE Sequence of a soluble form of the interferon (IFN) receptor with a high
DE affinity for IFN-alpha and -beta.
XX Interferon receptor; alpha-interferon; beta-interferon.
XX Synthetic.
XX WO9218626-A1.
XX
XX PD 29-OCT-1992.
XX
XX PF 17-APR-1991; 91WO-FR000318.
XX
XX PR 17-APR-1991; 91WO-FR000318.
XX
XX PA (EUBI-) LAB EURO BIOTECHNOLOGIE.
XX
XX PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;
XX Uze G;
XX WPI; 1992-382110/46.
XX DR N-PSDB; AAQ30532.
XX
XX PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -
XX useful as immunosuppressants, for treating auto-immune diseases and
XX transplant rejection.
XX Claim 2; Fig 1; 58pp; English.
XX
XX CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-
XX alpha and -beta is isolated by PCR, using appropriate oligonucleotides as
XX primers and cloned cDNA as template. For example, bacteriophage lambda
XX ZAP, containing the entire coding sequence of the IFN-alpha and -beta
```

```
CC receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.
CC AAR28495 represents the complete receptor. AAR28495 lacks the
CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same
CC way as antibodies so are immunosuppressants e.g. for treating autoimmune
CC diseases and graft rejection. They lack the toxic side-effects of known
CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 436 AA;
Query Match 100.0%; Score 2141; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.6e-184;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSCQNITSTK 60
DB 27 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSCQNITSTK 86
QY 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 120
DB 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 146
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLVKVKAAL 180
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLVKVKAAL 206
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLRVQASDGNNTSFWSSEIKFDT 240
DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLRVQASDGNNTSFWSSEIKFDT 266
QY 241 KRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300
DB 267 KRNPGNHLKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326
QY 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYETIIFWENTSNAERKIIIE 360
DB 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYETIIFWENTSNAERKIIIE 386
QY 361 KKTDTVTVPNLKPLTYCYVKARAHMTDEKLNKSSVFSDAVCE 401
DB 387 KKTDTVTVPNLKPLTYCYVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 3
ABU05090
ID ABU05090 standard; protein; 436 AA.
AC ABU05090;
XX
XX
DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1756.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX FN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
```

```
XX (ZYCO-) ZYCOS INC.
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1756; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (BPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 436 AA;
XX
XX Query Match 100.0%; Score 2141; DB 6; Length 436;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-184;
XX Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNTSTK 60
DB 27 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNTSTK 86
QY 61 CNFSSKLKNVYEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPPEVHLEADKAIVIH 120
DB 87 CNFSSKLKNVYEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPPEVHLEADKAIVIH 146
QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 180
DB 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 206
QY 181 LTSWKIGVSPVHCITTVENELPPDENIEVSQNVYLVKWDYTYANNFTFQVQMLHAPL 240
DB 207 LTSWKIGVSPVHCITTVENELPPDENIEVSQNVYLVKWDYTYANNFTFQVQMLHAPL 266
QY 241 KENPGNHLVKKQIPDCENVKTKTCVPFQNVKQGIYLLRQASDGNNTSFWSSEIKFPT 300
DB 267 KENPGNHLVKKQIPDCENVKTKTCVPFQNVKQGIYLLRQASDGNNTSFWSSEIKFPT 326
QY 301 EQIAFLPLPVFNIRSLSDSFHYIGAPKQSGNTPTVIQDYPLIYEIIFWNTSNARKIIE 360
DB 327 EQIAFLPLPVFNIRSLSDSFHYIGAPKQSGNTPTVIQDYPLIYEIIFWNTSNARKIIE 386
QY 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSVFSDAVCE 401
DB 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSVFSDAVCE 427
XX
RESULT 4
ABU05092
ID ABU05092 standard; protein; 436 AA.
XX
XX AC ABU05092;
XX
```

```
DT 29-JAN-2003 (first entry)
XX Human expressed protein tag (BPT) #1758.
XX Translational profiling; expressed protein tag; BPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX
XX Example 2; SEQ ID NO 1758; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (BPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 436 AA;
XX
XX Query Match 100.0%; Score 2141; DB 6; Length 436;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-184;
XX Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNTSTK 60
DB 27 GNKLSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNTSTK 86
QY 61 CNFSSKLKNVYEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPPEVHLEADKAIVIH 120
DB 87 CNFSSKLKNVYEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPPEVHLEADKAIVIH 146
QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 180
DB 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPTTYCLKVKAAL 206
QY 181 LTSWKIGVSPVHCITTVENELPPDENIEVSQNVYLVKWDYTYANNFTFQVQMLHAPL 240
DB 207 LTSWKIGVSPVHCITTVENELPPDENIEVSQNVYLVKWDYTYANNFTFQVQMLHAPL 266
QY 241 KENPGNHLVKKQIPDCENVKTKTCVPFQNVKQGIYLLRQASDGNNTSFWSSEIKFPT 300
DB 267 KENPGNHLVKKQIPDCENVKTKTCVPFQNVKQGIYLLRQASDGNNTSFWSSEIKFPT 326
QY 301 EQIAFLPLPVFNIRSLSDSFHYIGAPKQSGNTPTVIQDYPLIYEIIFWNTSNARKIIE 360
DB 327 EQIAFLPLPVFNIRSLSDSFHYIGAPKQSGNTPTVIQDYPLIYEIIFWNTSNARKIIE 386
QY 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSVFSDAVCE 401
DB 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSVFSDAVCE 427
XX
RESULT 4
ABU05092
ID ABU05092 standard; protein; 436 AA.
XX
XX AC ABU05092;
XX
```

QY 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVQWLHAPL 240  
DB 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVQWLHAPL 266  
QY 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
DB 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPVQDYPLIYEIIFWENTSNAERKIIIE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPVQDYPLIYEIIFWENTSNAERKIIIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 5  
ID ABU05098 standard; protein; 436 AA.  
AC ABU05098;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1764.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
FN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US0095671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX  
PA (ZYCO-) ZYCOS INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX  
DR WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1764; 134pp; English.  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,

CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 436 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 436;  
Best Local Similarity 100.0%; Pred. No. 1.6e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLKSPQKVEVDIIDDNFILRNWRSDESQNVTFSPDYQKTGMNDWIKLSCQNTITSTK 60  
DB 27 GKNLKSPQKVEVDIIDDNFILRNWRSDESQNVTFSPDYQKTGMNDWIKLSCQNTITSTK 86  
QY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEAEDKAIVIH 120  
DB 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPRKAOIGPPEVHLEAEDKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPEPTYCLKVKAAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPEPTYCLKVKAAAL 206  
QY 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVQWLHAPL 240  
DB 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANNMTFQVQWLHAPL 266  
QY 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
DB 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPVQDYPLIYEIIFWENTSNAERKIIIE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHIYIGAPKQSGNTPVQDYPLIYEIIFWENTSNAERKIIIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 6  
AAR14488  
ID AAR14488 standard; protein; 557 AA.  
XX  
AC AAR14488;  
XX  
DT 16-JAN-1992 (first entry)  
XX  
DE Complete interferon-alpha/beta receptor.  
XX  
KW IFN; autoimmune disease; graft rejection; histocompatibility.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 437..457  
FT /label= transmembrane  
FT Domain 458..557  
FT /label= cytoplasmic  
XX  
FN FR2657881-A.  
XX  
PD 09-AUG-1991.  
XX  
PF 05-FEB-1990; 90FR-00001298.  
XX  
PR 05-FEB-1990; 90FR-00001298.  
XX  
PA (EUBI-) LAB EURO BIOTECHNO.  
XX  
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey MG;



PI Use G;  
 XX WPI; 1991-319778/44.  
 DR N-PSDB; AAQ14240.  
 XX  
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
 PT used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
 PT anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
 XX  
 PS Disclosure; Page 47; 52pp; French.  
 XX  
 XX The invention covers derivatives of the interferon-alpha and/or beta  
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains  
 CC of the native receptor or by substitution. Potentially immunogenic  
 CC epitopes are eliminated and the deriv. can be secreted from transformed  
 CC cells. Soluble deriv.s block the activity of IFN alpha/beta and can be  
 CC used to treat autoimmune diseases or to inhibit graft rejection. See also  
 CC AAQ14239  
 XX  
 SQ Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GKNLSPQKVEVDIIDDNFILRNRSDESVGNVTFSDYQKTMGNWIKLSCGQNTSTK 60  
 Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESVGNVTFSDYQKTMGNWIKLSCGQNTSTK 86  
 QY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEAEKAIYIHI 120  
 Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEAEKAIYIHI 146  
 QY 121 SPGTGDSVNMALDGLSFTYSLIWNKSSGVEERIEIYSRHKIYKLSPTTYCLKYKAAL 180  
 Db 147 SPGTGDSVNMALDGLSFTYSLIWNKSSGVEERIEIYSRHKIYKLSPTTYCLKYKAAL 206  
 QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240  
 Db 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 266  
 QY 241 KENPGNHLYKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
 Db 267 KENPGNHLYKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
 QY 301 EIQAFLLPPVFNIRSLDSFHIYIGAPKSGNTPTQDYPLIYEIIFWNTSNAERKIIIE 360  
 Db 327 EIQAFLLPPVFNIRSLDSFHIYIGAPKSGNTPTQDYPLIYEIIFWNTSNAERKIIIE 386  
 QY 361 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 401  
 Db 387 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 427

RESULT 7  
 AAR11958  
 ID AAR11958 standard; protein; 557 AA.  
 XX  
 AC AAR11958;  
 XX  
 DT 18-JUL-1991 (first entry)  
 XX  
 DE Human alpha-interferon receptor protein.  
 XX  
 DE Human alpha IFN; IFN agonists; antiviral; anti tumour agent;  
 KW drug targeting.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..27  
 FT /label= signal peptide  
 XX

PN WO9105862-A.  
 XX  
 PD 02-MAY-1991.  
 XX  
 PF 20-OCT-1989; 89PR-00013770.  
 XX  
 PR 20-OCT-1989; 89PR-00013770.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 XX Mogensen K, Lutfalla G, Gresser I;  
 PI WPI; 1991-148740/20.  
 DR N-PSDB; AAQ11701.  
 XX  
 XX New human alpha-interferon receptor protein - useful for testing  
 PT interferon agonists and in treatment or diagnosis.  
 PT  
 XX  
 PS Disclosure; Fig 4; 30pp; French.  
 XX  
 CC This recombinant human alpha interferon (IFN) receptor protein is useful  
 CC for the testing of IFN agonists and for treatment and diag- nosis of  
 CC viral diseases and tumours. Antibodies raised against this protein can be  
 CC used for blocking the receptor when required, eg where overexpression of  
 CC alpha-IFN is harmful. The Abs are also useful for eg drug targeting.  
 CC Variants of the protein, having residue 164 (Thr) replaced by Arg and an  
 CC Asp inserted between residues 479 and 480, are also useful  
 XX  
 SQ Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GKNLSPQKVEVDIIDDNFILRNRSDESVGNVTFSDYQKTMGNWIKLSCGQNTSTK 60  
 Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESVGNVTFSDYQKTMGNWIKLSCGQNTSTK 86  
 QY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEAEKAIYIHI 120  
 Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFRAQIGPPEVHLEAEKAIYIHI 146  
 QY 121 SPGTGDSVNMALDGLSFTYSLIWNKSSGVEERIEIYSRHKIYKLSPTTYCLKYKAAL 180  
 Db 147 SPGTGDSVNMALDGLSFTYSLIWNKSSGVEERIEIYSRHKIYKLSPTTYCLKYKAAL 206  
 QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240  
 Db 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 266  
 QY 241 KENPGNHLYKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
 Db 267 KENPGNHLYKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
 QY 301 EIQAFLLPPVFNIRSLDSFHIYIGAPKSGNTPTQDYPLIYEIIFWNTSNAERKIIIE 360  
 Db 327 EIQAFLLPPVFNIRSLDSFHIYIGAPKSGNTPTQDYPLIYEIIFWNTSNAERKIIIE 386  
 QY 361 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 401  
 Db 387 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 427

RESULT 8  
 AAR28496  
 ID AAR28496 standard; protein; 557 AA.  
 XX  
 AC AAR28496;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 31-MAR-1993 (first entry)  
 XX  
 DE Sequence of a soluble form of the interferon (IFN) receptor with a high

DE affinity for IFN-alpha and -beta.  
 XX Interferon receptor; alpha-interferon; beta-interferon.  
 KW Synthetic.  
 OS WO9218626-A1.  
 PN 29-OCT-1992.  
 PD 17-APR-1991; 91WO-FR000318.  
 PF 17-APR-1991; 91WO-FR000318.  
 PG 17-APR-1991; 91WO-FR000318.  
 PH (EUBI-) LAB EURO BIOTECHNOLOGIE.  
 PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
 PZ Uze G;  
 DR WPI: 1992-382110/46.  
 DR N-PSDB; AAQ30533.  
 XX Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
 PT useful as immunosuppressants, for treating autoimmune diseases and  
 PT transplant rejection.  
 XX Claim 3; Fig 2; 59pp; English.  
 XX DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
 CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
 CC primers and cloned cDNA as template. For example, bacteriophage lambda  
 CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
 CC receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.  
 CC AAR28496 represents the complete receptor. AAR28495 lacks the  
 CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
 CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
 CC diseases and graft rejection. They lack the toxic side-effects of known  
 CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX Sequence 557 AA;  
 SQ Query Match 100.0%; Score 2141; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-184; Mismatches 0; Indels 0; Gaps 0;  
 Matches 401; Conservative 0;  
 QY 1 GNKLSPQKVEVDIIDDNFILWNRSDSVGNVTFSDYQKTGMNDNWLKSGCQNTSTK 60  
 DB 27 GNKLSPQKVEVDIIDDNFILWNRSDSVGNVTFSDYQKTGMNDNWLKSGCQNTSTK 86  
 QY 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 120  
 DB 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 146  
 QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVSEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
 DB 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVSEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
 QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLKWDYTYANNFTQVQWLHAF 240  
 DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLKWDYTYANNFTQVQWLHAF 266  
 QY 241 KNPNGHLYKWQIQIDPCENVKTTQCVFPQNVQKGIYLLRQVSDGNNTSPWSEIKFDT 300  
 DB 267 KNPNGHLYKWQIQIDPCENVKTTQCVFPQNVQKGIYLLRQVSDGNNTSPWSEIKFDT 326  
 QY 301 EQAFLLPPVFNIRSLSDSFHYIIGAPKOSGNTPVQDYPLIYELIIPWENTSNAERKIE 360  
 DB 327 EQAFLLPPVFNIRSLSDSFHYIIGAPKOSGNTPVQDYPLIYELIIPWENTSNAERKIE 386  
 QY 361 KKTDTVFNLPKLTIVYCVKARAHTMDEKLNKSSVFSVDAVCE 401  
 DB 387 KKTDTVFNLPKLTIVYCVKARAHTMDEKLNKSSVFSVDAVCE 427

RESULT 9  
 AAR42635  
 ID AAR42635 standard; protein; 557 AA.  
 XX AAR42635;  
 AC AAR42635;  
 XX 25-MAR-2003 (revised)  
 DT 20-APR-1994 (first entry)  
 XX Human interferon receptor.  
 DE IFN-R; extracellular domain; monoclonal antibody; viral infection;  
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;  
 KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;  
 KW immunodeficiency; measles virus; interferon-alpha-beta.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Domain 1.436  
 FT /label= extracellular domain  
 FT /note= "soluble, immunogenic form of IFN-R"  
 XX EP563487-A1.  
 XX 06-OCT-1993.  
 XX 31-MAR-1992; 92EP-00400902.  
 XX 31-MAR-1992; 92EP-00400902.  
 XX (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 XX Benoit P, Meyer F, Maguire D, Plavec I, Tovey MG;  
 XX WPI: 1993-312951/40.  
 DR P-PSDB; AAR42635.  
 XX Monoclonal antibody to human interferon type-I receptor - having  
 PT neutralising activity against human type I interferon, used for therapy  
 PT and diagnosis.  
 XX Disclosure; Fig 3; 21pp; English.  
 XX Monoclonal antibodies produced against soluble forms of the human  
 CC interferon alpha-beta receptor based on the full-length human IFN-R  
 CC sequence are claimed. The antibodies are useful for treatment and  
 CC prophylaxis of disorders involving cell proliferation and/or viral  
 CC infection. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 557 AA;  
 SQ Query Match 100.0%; Score 2141; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-184; Mismatches 0; Indels 0; Gaps 0;  
 Matches 401; Conservative 0;  
 QY 1 GNKLSPQKVEVDIIDDNFILWNRSDSVGNVTFSDYQKTGMNDNWLKSGCQNTSTK 60  
 DB 27 GNKLSPQKVEVDIIDDNFILWNRSDSVGNVTFSDYQKTGMNDNWLKSGCQNTSTK 86  
 QY 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 120  
 DB 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHI 146  
 QY 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVSEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
 DB 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVSEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
 QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLKWDYTYANNFTQVQWLHAF 240  
 DB 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQNYVLKWDYTYANNFTQVQWLHAF 266

```
QY 241 KNPNGNHLKWKQIIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFSEIEIKFDT 300
DB 267 KNPNGNHLKWKQIIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFSEIEIKFDT 326
QY 301 EIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIIE 360
DB 327 EIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIIE 386
QY 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401
DB 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 10
ABU05091
ID ABU05091 standard; protein; 557 AA.
XX AC ABU05091;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1757.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX PS Example 2; SEQ ID NO 1757; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
```

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CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 557 AA;
Query Match 100.0%; Score 2141; DB 6; Length 557;
Best Local Similarity 100.0%; Pred. No. 2.2e-184;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKNLAKSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMONWIKLSGQNITSTK 60
DB 27 GKNLAKSPQKVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMONWIKLSGQNITSTK 86
QY 61 CNFSSILKLNVEEIKLIRAEKENTSSWYEVDSTFPRKQAQIGPPEVHLEADKAIVIH 120
DB 87 CNFSSILKLNVEEIKLIRAEKENTSSWYEVDSTFPRKQAQIGPPEVHLEADKAIVIH 146
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSGVBERIENIYSRHKIYKLSPTTYCLKYKAAL 180
DB 147 SPGTKDSVMWALDGLSFTYSLLIWNKSGVBERIENIYSRHKIYKLSPTTYCLKYKAAL 206
QY 181 LTSWKIGVYSPVHCJKTTVENELPPENIEVSQNVQNYLVKWDYTYANNMTFOVQWLHAF 240
DB 207 LTSWKIGVYSPVHCJKTTVENELPPENIEVSQNVQNYLVKWDYTYANNMTFOVQWLHAF 266
QY 241 KNPNGNHLKWKQIIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFSEIEIKFDT 300
DB 267 KNPNGNHLKWKQIIPDCENVKTKTCVFPQNVFQKGIYLLRVQASDGNNTSFSEIEIKFDT 326
QY 301 EIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIIE 360
DB 327 EIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIFWNTSNAERKIIIE 386
QY 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401
DB 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 11
ABU05095
ID ABU05095 standard; protein; 557 AA.
XX AC ABU05095;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1761.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX
```

DR WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX  
PS Example 2; SEQ ID NO 1761; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184; Indels 0; Gaps 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILWRNRSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILWRNRSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTSLIWKNSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTSLIWKNSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNYVLYKWDYTYANNMTFQVWLHAPL 240  
Db 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNYVLYKWDYTYANNMTFQVWLHAPL 266  
QY 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSPWSEIKFT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVQASDGNNTSPWSEIKFT 326  
QY 301 ETQAFLLPVPFNIRSLDSFHYIGAPKQSGNTPTVTDYPLIYEIIFWNTSNAERKIE 360  
Db 327 ETQAFLLPVPFNIRSLDSFHYIGAPKQSGNTPTVTDYPLIYEIIFWNTSNAERKIE 386  
QY 361 KKTDTVTPNLKPLTVYCVKARHTMDKLNKSVFSDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARHTMDKLNKSVFSDAVCE 427

RESULT 12  
ID ABU05094  
XX ABU05094 standard; protein; 557 AA.  
AC ABU05094;  
XX  
XX 29-JAN-2003 (first entry)  
DT  
XX Human expressed protein tag (EPT) #1760.  
XX  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
OS Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US009671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
XX 21-MAY-2001; 2001US-0292544P.  
XX 08-AUG-2001; 2001US-0310801P.  
XX 01-OCT-2001; 2001US-0326370P.  
XX 04-DEC-2001; 2001US-0336780P.  
XX 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCO INC.  
XX  
XX Chicx RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1760; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;

Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184; Indels 0; Gaps 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILWRNRSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILWRNRSDESGVNTFSFDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTSLIWKNSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTSLIWKNSGVEERENIYSRHKIYKLSPTTYCLVKVKAAL 206  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNYVLYKWDYTYANNMTFQVWLHAPL 240  
Db 207 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNYVLYKWDYTYANNMTFQVWLHAPL 266

QY 241 KRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQKGIYLLRVQASDGNNTSFWSBEIKPDT 300  
DB 267 KRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQKGIYLLRVQASDGNNTSFWSBEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIFWENTSNARKKITE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIFWENTSNARKKITE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 427

RESULT 13  
ID ABU05107 standard; protein; 557 AA.  
AC ABU05107;  
XX  
DT 29-JAN-2003 (first entry)  
XX Human expressed protein tag (EPT) #1773.  
DE Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX Homo sapiens.  
XX  
PN WO200278524-A2.  
XX 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCOS INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1773; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKQVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNTITSTK 60  
DB 27 GKNLSPQKQVEVDIIDDNPFILWNRSDSVGNVTFSDYQKTGMNDWIKLSCQNTITSTK 86  
QY 61 CNFSSLKLNVYBEIKLIRAEKENTSSWYEDVSTPFRKAQIGPPEVHLEASDKAIVIH 120  
DB 87 CNFSSLKLNVYBEIKLIRAEKENTSSWYEDVSTPFRKAQIGPPEVHLEASDKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLIWNSSGVEERIENIYSRHKIYKLSPTTTCYLVKKAAL 180  
DB 147 SPGTKDSVMWALDGLSFTYSLIWNSSGVEERIENIYSRHKIYKLSPTTTCYLVKKAAL 206  
QY 181 LTSWKIGYVSPVHCIKTTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQMLHAF 240  
DB 207 LTSWKIGYVSPVHCIKTTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQMLHAF 266  
QY 241 KRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQKGIYLLRVQASDGNNTSFWSBEIKPDT 300  
DB 267 KRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQKGIYLLRVQASDGNNTSFWSBEIKPDT 326  
QY 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIFWENTSNARKKITE 360  
DB 327 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTPVQIDYPLIYEIFWENTSNARKKITE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTVPNLKPLTVYCVKARAHMTWDEKLNKSSVFSDAVCE 427

RESULT 14  
ABU05099  
ID ABU05099 standard; protein; 557 AA.  
XX  
AC ABU05099;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1765.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US009671.  
XX  
PR 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCOS INC.  
XX  
PI Chicx RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1765; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 557 AA;  
XX  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 266  
QY 241 KENPGNHLKWKQIIPDCENVKTTCQVFPQNVFQKGIYLLRVQASDGNNTSFWSEIKFDT 300  
Db 267 KENPGNHLKWKQIIPDCENVKTTCQVFPQNVFQKGIYLLRVQASDGNNTSFWSEIKFDT 326  
QY 301 EIQAFLPPVFNIRSLDSFHYICAPKQSGNTPTVIQDYPLIYEIIFWENTSNAERKIIIE 360  
Db 327 EIQAFLPPVFNIRSLDSFHYICAPKQSGNTPTVIQDYPLIYEIIFWENTSNAERKIIIE 386  
QY 361 KKTDTVTNKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTNKLPLTYCYVKARAHTMDEKLNKSSVFSDAVCE 427  
RESULT 15  
ABU05106  
ID ABU05106 standard; protein; 557 AA.  
XX  
AC ABU05106;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1772.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
OS Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX 10-OCT-2002.  
XX  
XX 28-MAR-2002; 2002WO-US009671.  
XX  
XX 28-MAR-2001; 2001US-0279495P.  
XX  
XX 21-MAY-2001; 2001US-0292544P.  
XX  
XX 08-AUG-2001; 2001US-0310801P.  
XX  
XX 01-OCT-2001; 2001US-0326370P.  
XX  
XX 04-DEC-2001; 2001US-0336780P.  
XX  
XX 20-FEB-2002; 2002US-0358985P.  
XX  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chiciz RM, Tomlinson AJ, Urban RG;  
XX  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1772; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 557 AA;  
XX  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GNKLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEADKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
QY 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSQNVQYVLDYTYANMTFQVQWLHAF 266  
QY 241 KENPGNHLKWKQIIPDCENVKTTCQVFPQNVFQKGIYLLRVQASDGNNTSFWSEIKFDT 300

Db 267 KENPGNHLKWKQIPDCENVTTCVFPQNVFQKGIYLLRVQASDGNNTSFNSEIKPDT 326  
QY 301 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYEIIFWENTSNARKIIE 360  
Db 327 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYEIIFWENTSNARKIIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTWDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTVPNLKPLTVYCVKARAHTWDEKLNKSSVFSDAVCE 427

RESULT 16  
ABU05097  
ID ABU05097 standard; protein; 557 AA.  
XX AC ABU05097;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1763.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chiciz RM, Tomlinson AJ, Urban RG;  
XX DR WPI; 2003-040607/03.  
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX PS Example 2; SEQ ID NO 1763; 134pp; English.  
XX CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 557 AA;  
Query Match 100.0%; Score 2141; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e-184; Mismatches 0; Indels 0; Gaps 0;  
Matches 401; Conservative 0;  
QY 1 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYQKTGMNDWIKLSCQNITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSFDYQKTGMNDWIKLSCQNITSTK 86  
QY 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEARDKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTFPRKAQIGPPEVHLEARDKAIVIH 146  
QY 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENYSRHKIYKLSPTTTCVLYKAAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERIENYSRHKIYKLSPTTTCVLYKAAAL 206  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPPELVSVQNTYVLKWDYTYANNFTQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPELVSVQNTYVLKWDYTYANNFTQVQWLHAF 266  
QY 241 KENPGNHLKWKQIPDCENVTTCVFPQNVFQKGIYLLRVQASDGNNTSFNSEIKPDT 300  
Db 267 KENPGNHLKWKQIPDCENVTTCVFPQNVFQKGIYLLRVQASDGNNTSFNSEIKPDT 326  
QY 301 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYEIIFWENTSNARKIIE 360  
Db 327 EQAFLPLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYEIIFWENTSNARKIIE 386  
QY 361 KKTDTVTVPNLKPLTVYCVKARAHTWDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTVPNLKPLTVYCVKARAHTWDEKLNKSSVFSDAVCE 427

RESULT 17  
ABU05093  
ID ABU05093 standard; protein; 557 AA.  
XX AC ABU05093;  
XX DT 29-JAN-2003 (first entry)  
XX DE Human expressed protein tag (EPT) #1759.  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX OS Homo sapiens.  
XX PN WO200278524-A2.  
XX PD 10-OCT-2002.  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX PA (ZYCO-) ZYCOS INC.  
XX PI Chiciz RM, Tomlinson AJ, Urban RG;  
XX DR WPI; 2003-040607/03.  
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX PS Example 2; SEQ ID NO 1763; 134pp; English.  
XX CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences





Db 267 KRNPGNHLKWKQIPDCENVKTTQCVPQNVFKGIYLLRVQASDGNNTSPWSEBIKPT 326  
Qy 301 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWENTNAERKIIIE 360  
Db 327 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWENTNAERKIIIE 386  
Qy 361 KKTDTVTPNLPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTPNLPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 427

RESULT 19  
ADR666319  
ID ADR666319 standard; protein; 575 AA.  
XX ADR666319;  
AC ADR666319;  
XX  
DT 02-DEC-2004 (first entry)  
XX Human prostatic carcinoma derived protein SEQ ID 173 #2.  
DE  
XX human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004076614-A2.  
XX  
PD 10-SEP-2004.  
XX  
PF 22-FEB-2004; 2004WO-DE000433.  
XX  
PR 27-FEB-2003; 2003DE-01009985.  
PR 14-MAY-2003; 2003DE-01022134.  
XX  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILAR/) PILARSKY C.  
XX  
PI Hinzmänn B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
PI Xinzhong L, Staub E;  
XX  
WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX  
XX Claim 2; Page 653; 1607pp; German.  
XX  
XX This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotype, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from

CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.  
XX  
SQ Sequence 575 AA;

Query Match 100.0%; Score 2141; DB 8; Length 575;  
Best Local Similarity 100.0%; Pred. No. 2.3e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GKNLKSPOKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTMGNWIKLSCQNITSTK 60  
Db 45 GKNLKSPOKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTMGNWIKLSCQNITSTK 104  
Qy 61 CNFSSLKLNVEBEIKLIRAEKENTSSWYEVDSFTFPRKAIQGPPEVHLEAEDKAIVIH 120  
Db 105 CNFSSLKLNVEBEIKLIRAEKENTSSWYEVDSFTFPRKAIQGPPEVHLEAEDKAIVIH 164  
Qy 121 SPGTKDSVMWALDGLSFTYSLIWKNSGVEERIENISRHKIYKLSPTTYCLKVKAAAL 180  
Db 165 SPGTKDSVMWALDGLSFTYSLIWKNSGVEERIENISRHKIYKLSPTTYCLKVKAAAL 224  
Qy 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVNVLKWDYTYANNMTFQVQLHAF 240  
Db 225 LTSWKIGVYSPVHCIKTTVENELPPENIEVSQNVNVLKWDYTYANNMTFQVQLHAF 284  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVPQNVFKGIYLLRVQASDGNNTSPWSEBIKPT 300  
Db 285 KRNPGNHLKWKQIPDCENVKTTQCVPQNVFKGIYLLRVQASDGNNTSPWSEBIKPT 344  
Qy 301 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWENTNAERKIIIE 360  
Db 345 EIQAFLLPPVFNIRSLDSFHIYIGAPKOSGNTPIQDYPLIYEIIFWENTNAERKIIIE 404  
Qy 361 KKTDTVTPNLPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 401  
Db 405 KKTDTVTPNLPKPLTYVCVKARAHMTWDEKLNKSSVFSDAVCE 445

RESULT 20

ADR666661  
ID ADR666661 standard; protein; 575 AA.  
XX ADR666661;  
AC ADR666661;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human prostatic carcinoma derived protein SEQ ID 173 #3.  
XX  
KW human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004076614-A2.  
XX  
PD 10-SEP-2004.  
XX  
PF 22-FEB-2004; 2004WO-DE000433.  
XX  
PR 27-FEB-2003; 2003DE-01009985.  
PR 14-MAY-2003; 2003DE-01022134.  
XX  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
XX  
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
PI Kinzhong L, Staub E;  
XX  
DR WPI; 2004-653386/63.  
XX  
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX  
PS Claim 2; Page 1155; 1607pp; German.  
XX

Search completed: January 18, 2006, 06:28:56  
Job time : 80 secs

This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR6805-ADR6954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 575 AA;  
Query Match 100.0%; Score 2141; DB 8; Length 575;  
Best Local Similarity 100.0%; Pred. No. 2.3e-184;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLSPQKVEVDIIDDNFILRWNRSDSGVGNVTFSDYQKTGMNDWIKLSCQNITSTK 60  
DB 45 GKNLSPQKVEVDIIDDNFILRWNRSDSGVGNVTFSDYQKTGMNDWIKLSCQNITSTK 104  
QY 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFKRAQIGPPEVHLEADKAIVIH 120  
DB 105 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPFKRAQIGPPEVHLEADKAIVIH 164  
QY 121 SPGTKDSVNMWALDGLSFTYSLIWKNSGVEERIEIYSRHKIYKLSPTTYCLKVKAAL 180  
DB 165 SPGTKDSVNMWALDGLSFTYSLIWKNSGVEERIEIYSRHKIYKLSPTTYCLKVKAAL 224  
QY 181 LTSWKIGVYSPVHCIKTTVENELPPENIEVSVQNVYLVKWDYTYANNFTQVOMLHAPL 240  
DB 225 LTSWKIGVYSPVHCIKTTVENELPPENIEVSVQNVYLVKWDYTYANNFTQVOMLHAPL 284  
QY 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVOASDGNNTSFWSEIKFDT 300  
DB 285 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGIYLLRVOASDGNNTSFWSEIKFDT 344  
QY 301 EIQAFLLPVPFNIRSLSDSFHIYIGAPKQSGNTPVQDYPLIYEIFWENTSNAERKII 360

DB 345 EIQAFLLPVPFNIRSLSDSFHIYIGAPKQSGNTPVQDYPLIYEIFWENTSNAERKII 404  
QY 361 KKTDTVTNPKPLTVYCVKARAHWTDEKLNKSSVFSFSDAVCE 401  
DB 405 KKTDTVTNPKPLTVYCVKARAHWTDEKLNKSSVFSFSDAVCE 445

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:18:53 ; Search time 81.4456 Seconds

(without alignments)

2057.195 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427

Perfect score: 2141

Sequence: 1 GKNLKSPQKEVDIIDNFI.....AHTMDEKLNKSSVPSDAVCE 401

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pap.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	436	3	US-09-240-675-2
2	2141	100.0	436	4	US-10-824-981-2
3	2141	100.0	436	5	US-10-473-127-1756
4	2141	100.0	436	5	US-10-473-127-1758
5	2141	100.0	436	5	US-10-473-127-1764
6	2141	100.0	557	3	US-09-240-675-4
7	2141	100.0	557	4	US-10-358-228-3
8	2141	100.0	557	5	US-10-473-127-1757
9	2141	100.0	557	5	US-10-473-127-1759
10	2141	100.0	557	5	US-10-473-127-1760
11	2141	100.0	557	5	US-10-473-127-1761
12	2141	100.0	557	5	US-10-473-127-1763
13	2141	100.0	557	5	US-10-473-127-1765
14	2141	100.0	557	5	US-10-473-127-1766
15	2141	100.0	557	5	US-10-473-127-1772
16	2141	100.0	557	5	US-10-473-127-1773
17	2138	99.9	441	5	US-10-764-833-41
18	2137	99.8	557	5	US-10-473-127-1768
19	2136	99.8	434	5	US-10-473-127-1770
20	2136	99.8	557	4	US-10-824-981-4
21	2136	99.8	557	5	US-10-473-127-1769
22	2136	99.8	575	3	US-09-925-300-1672
23	2136	99.8	575	5	US-10-473-127-1762
24	2136	99.8	575	5	US-10-450-763-47653
25	2136	99.6	436	5	US-10-473-127-1767
26	2084	97.3	496	5	US-10-473-127-1771
27	1384.5	64.7	560	4	US-10-293-832-29

Sequence 30, Appl  
Sequence 33, Appl  
Sequence 15, Appl  
Sequence 14, Appl  
Sequence 19, Appl  
Sequence 44, Appl  
Sequence 2, Appl  
Sequence 8, Appl  
Sequence 23, Appl  
Sequence 62, Appl  
Sequence 63, Appl  
Sequence 62, Appl  
Sequence 16, Appl  
Sequence 3, Appl  
Sequence 5, Appl  
Sequence 390, App  
Sequence 137, App  
Sequence 390, App

28 1377.5 64.3 560 4 US-10-293-832-30  
29 488.5 22.8 198 4 US-10-293-832-33  
30 228 10.6 273 4 US-10-186-180-13  
31 226 10.6 273 4 US-10-186-180-14  
32 225 10.5 220 3 US-09-925-055D-19  
33 225 10.5 220 4 US-10-807-837-44  
34 225 10.5 273 4 US-10-186-180-2  
35 225 10.5 273 4 US-10-358-228-8  
36 225 10.5 476 3 US-09-925-055D-23  
37 225 10.5 476 4 US-10-104-919-62  
38 225 10.5 476 4 US-10-395-741B-63  
39 225 10.5 476 5 US-10-968-432-62  
40 224 10.5 273 4 US-10-186-180-16  
41 220 10.3 325 3 US-09-870-574-3  
42 220 10.3 325 3 US-09-949-192-5  
43 220 10.3 325 4 US-10-052-586-390  
44 220 10.3 325 4 US-10-066-500-137  
45 220 10.3 325 4 US-10-174-590-390

#### ALIGNMENTS

#### RESULT 1

US-09-240-675-2

; Sequence 2, Application US/09240675

; Patent No. US20020055492A1

; GENERAL INFORMATION:

; APPLICANT: BENOIT, Patrick

; APPLICANT: MEYER, Francois

; APPLICANT: MAGUIRE, Deborah

; APPLICANT: FLAVEC, Ivan

; APPLICANT: TOVEY, Michael G.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA: 675

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/307,588

; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: PCT/EP93/00770

; FILING DATE: 30-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 92400902.0

; FILING DATE: 31-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: SAXE, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 17283/117/GUPL

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 436 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-240-675-2

Query Match 100.0%; Score 2141; DB 3; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDES VGNVTFSPDYQKTGMDNWKLSGCCQNIITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDES VGNVTFSPDYQKTGMDNWKLSGCCQNIITSTK 86

Qy 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIIVHI 120  
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIIVHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPETTYCLKVKAAAL 206

Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONVYLKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONVYLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSPWSEIEKFD 300  
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSPWSEIEKFD 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVIQDYPLIYIIIFWENTSNAERKIE 360  
Db 327 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVIQDYPLIYIIIFWENTSNAERKIE 386

Qy 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 2  
US-10-824-981-2  
; Sequence 2, Application US/10824981  
; Publication No. US20040191840A1  
; GENERAL INFORMATION:  
; APPLICANT: Benoit, Patrick  
; APPLICANT: Meguire, Deborah  
; APPLICANT: Plavec, Ivan  
; APPLICANT: Tovy, Michael  
; APPLICANT: Meyer, Francois  
; TITLE OF INVENTION: Monoclonal Antibodies Against The Interferon Receptor, With  
; FILE REFERENCE: A-7230-2  
; CURRENT APPLICATION NUMBER: US/10/824,981  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US 09/240,675  
; PRIOR FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: US 08/307,588  
; PRIOR FILING DATE: 1994-12-05  
; PRIOR APPLICATION NUMBER: PCT/EP93/00770  
; PRIOR FILING DATE: 1993-03-30  
; PRIOR APPLICATION NUMBER: EP 92400902.0  
; PRIOR FILING DATE: 1992-03-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-824-981-2

Query Match 100.0%; Score 2141; DB 4; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDES VGNVTFSPDYQKTGMDNWKLSGCCQNIITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDES VGNVTFSPDYQKTGMDNWKLSGCCQNIITSTK 86

Qy 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIIVHI 120  
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIIVHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPETTYCLKVKAAAL 206

Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONVYLKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONVYLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSPWSEIEKFD 300  
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSPWSEIEKFD 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVIQDYPLIYIIIFWENTSNAERKIE 360  
Db 327 EIOAFLPPVFNIRSLSDSFHIIYIGAPKQSGNTFVIQDYPLIYIIIFWENTSNAERKIE 386

Qy 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 3  
US-10-473-127-1756  
; Sequence 1756, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1756  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1756

Query Match 100.0%; Score 2141; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDES VGNVTFSPDYQKTGMDNWKLSGCCQNIITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDES VGNVTFSPDYQKTGMDNWKLSGCCQNIITSTK 86

Qy 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIIVHI 120  
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAIIVHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIEIENYSRHKIYKLSPETTYCLKVKAAAL 206

Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONVYLKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONVYLKWDYTYANMTFQVQWLHAF 266

Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVVLKWDYTYANMTFQVQWLHAPL 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
Qy 301 EQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWNTSNAERKIIIE 360  
Db 327 EQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWNTSNAERKIIIE 386  
Qy 361 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSVDACE 401  
Db 387 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSVDACE 427

## RESULT 4

US-10-473-127-1758  
; Sequence 1758, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1758  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1758

Query Match 100.0%; Score 2141; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSGCONITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSGCONITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWVEVDSFTPPRKAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWVEVDSFTPPRKAQIGPPEVHLEADKAIVIH 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIEIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIEIYSRHKIYKLSPTTYCLVKVKAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVVLKWDYTYANMTFQVQWLHAPL 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVVLKWDYTYANMTFQVQWLHAPL 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
Qy 301 EQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWNTSNAERKIIIE 360  
Db 327 EQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWNTSNAERKIIIE 386

## RESULT 6

US-09-240-675-4  
; Sequence 4, Application US/09240675  
; Patent No. US20020055492A1  
; GENERAL INFORMATION:

Qy 361 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSVDACE 401  
Db 387 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSVDACE 427

## RESULT 5

US-10-473-127-1764  
; Sequence 1764, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1764  
; LENGTH: 436  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1764

Query Match 100.0%; Score 2141; DB 5; Length 436;  
Best Local Similarity 100.0%; Pred. No. 3e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSGCONITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESQVNTFSFDYQKTGMNDWIKLSGCONITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWVEVDSFTPPRKAQIGPPEVHLEADKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWVEVDSFTPPRKAQIGPPEVHLEADKAIVIH 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIEIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIEIYSRHKIYKLSPTTYCLVKVKAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVVLKWDYTYANMTFQVQWLHAPL 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNVVLKWDYTYANMTFQVQWLHAPL 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326  
Qy 301 EQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWNTSNAERKIIIE 360  
Db 327 EQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPVQDYPLIYELIIFWNTSNAERKIIIE 386  
Qy 361 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSVDACE 401  
Db 387 KKTDTVTVNLKPLTVYCVKARAHMTDEKLNKSSVFSVDACE 427

APPLICANT: BENOIT, Patrick  
APPLICANT: MEYER, Francois  
APPLICANT: MAGUIRE, Deborah  
APPLICANT: PLAVEC, Ivan  
APPLICANT: TOVEY, Michael G.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
TITLE OF INVENTION: INTERFERON  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,675  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-240-675-4

Query Match 100.0%; Score 2141; DB 3; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYOKTGMNDNWKLSGCONITSTK 60  
Db 27 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYOKTGMNDNWKLSGCONITSTK 86

Qy 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPPEVHLEADKAIIVHI 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPPEVHLEADKAIIVHI 146

Qy 121 SPGKDSVMWALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGKDSVMWALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206

Qy 181 LSWKIGVSPVHCITKTVENELPPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 240  
Db 207 LSWKIGVSPVHCITKTVENELPPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326

Qy 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPLIYEIFWNTSNAERKIIIE 360  
Db 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPLIYEIFWNTSNAERKIIIE 386

Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDKLNKSSVFSFSDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDKLNKSSVFSFSDAVCE 427

## RESULT 7

US-10-358-228-3  
Sequence 3, Application US/10358228  
Publication No. US20030211578A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc. et al.  
TITLE OF INVENTION: Interferon Receptor HKABF92  
FILE REFERENCE: PF465C1  
CURRENT APPLICATION NUMBER: US/10/358,228  
CURRENT FILING DATE: 2003-02-05  
PRIOR APPLICATION NUMBER: 09/453,569  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: 09/326,216  
PRIOR FILING DATE: 1999-06-03  
PRIOR APPLICATION NUMBER: 60/088,185  
PRIOR FILING DATE: 1998-06-05  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 557  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-358-228-3

Query Match 100.0%; Score 2141; DB 4; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYOKTGMNDNWKLSGCONITSTK 60  
Db 27 GKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSPDYOKTGMNDNWKLSGCONITSTK 86

Qy 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPPEVHLEADKAIIVHI 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPPEVHLEADKAIIVHI 146

Qy 121 SPGKDSVMWALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
Db 147 SPGKDSVMWALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206

Qy 181 LSWKIGVSPVHCITKTVENELPPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 240  
Db 207 LSWKIGVSPVHCITKTVENELPPPENIEVSQNVQNYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326

Qy 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPLIYEIFWNTSNAERKIIIE 360  
Db 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVQDYPLIYEIFWNTSNAERKIIIE 386

## RESULT 8

US-10-473-127-1757  
Sequence 1757, Application US/10473127  
Publication No. US20040236091A1  
GENERAL INFORMATION:  
APPLICANT: Zycos Inc.  
TITLE OF INVENTION: TRANSLATIONAL PROFILING  
FILE REFERENCE: 08191-026W01  
CURRENT APPLICATION NUMBER: US/10/473,127  
CURRENT FILING DATE: 2003-09-26

```
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1757
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1757

Query Match      100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESNGVTFFSDYQKTGMDNWKLSGCCQNIITSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESNGVTFFSDYQKTGMDNWKLSGCCQNIITSTK 86
Qy 61 CNFSSLLKNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEADKAIYIHI 120
Db 87 CNFSSLLKNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEADKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAAL 206
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNYVQLKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNYVQLKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPENHLYKWQIIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 300
Db 267 KRNPENHLYKWQIIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 326
Qy 301 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 360
Db 327 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 386
Qy 361 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 9
US-10-473-127-1759
; Sequence 1759, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1757
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1759
```

```
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1759
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1759

Query Match      100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESNGVTFFSDYQKTGMDNWKLSGCCQNIITSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESNGVTFFSDYQKTGMDNWKLSGCCQNIITSTK 86
Qy 61 CNFSSLLKNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEADKAIYIHI 120
Db 87 CNFSSLLKNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEADKAIYIHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAAL 206
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNYVQLKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNYVQLKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPENHLYKWQIIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 300
Db 267 KRNPENHLYKWQIIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSEIKPDT 326
Qy 301 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 360
Db 327 EIOAFLPPVFNIRSLSDSFHIYIGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 386
Qy 361 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVPNLKPLTYVCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 10
US-10-473-127-1760
; Sequence 1760, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1760
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1760
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Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESGVNTFSDYQKTGMDNWKLSGCCNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESGVNTFSDYQKTGMDNWKLSGCCNITSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 120  
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy 181 LTSWKIGVSPVHCICKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVSPVHCICKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWNTSNAERKII E 360  
Db 327 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWNTSNAERKII E 386

Qy 361 KKTDTVPNLKLPTVYCVKARAHTMDKLNKSSVFSDAVCE 401  
Db 387 KKTDTVPNLKLPTVYCVKARAHTMDKLNKSSVFSDAVCE 427

## RESULT 11

US-10-473-127-1761  
; Sequence 1761, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1761  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1761

Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESGVNTFSDYQKTGMDNWKLSGCCNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESGVNTFSDYQKTGMDNWKLSGCCNITSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 120

Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180

Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy 181 LTSWKIGVSPVHCICKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 240

Db 207 LTSWKIGVSPVHCICKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 266

Qy 241 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300

Db 267 KRNPGNHLXKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326

Qy 301 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWNTSNAERKII E 360

Db 327 EIOAFLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWNTSNAERKII E 386

Qy 361 KKTDTVPNLKLPTVYCVKARAHTMDKLNKSSVFSDAVCE 401

Db 387 KKTDTVPNLKLPTVYCVKARAHTMDKLNKSSVFSDAVCE 427

## RESULT 12

US-10-473-127-1763  
; Sequence 1763, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; PRIOR FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1763  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1763

Query Match 100.0%; Score 2141; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 4.2e-182;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDDNFILRNRSDESGVNTFSDYQKTGMDNWKLSGCCNITSTK 60  
Db 27 GKNLKSQKVEVDIIDDNFILRNRSDESGVNTFSDYQKTGMDNWKLSGCCNITSTK 86

Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 120

Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180

Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy 181 LTSWKIGVSPVHCICKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 240

Db 207 LTSWKIGVSPVHCICKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 266



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Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFQNGYVFKGIYLLRVOASDGNNTFSWSEIKEDT 300
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFQNGYVFKGIYLLRVOASDGNNTFSWSEIKEDT 326
Qy 301 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYELIIFWENTSNARKEIIE 360
Db 327 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYELIIFWENTSNARKEIIE 386
Qy 361 KKTDTVTNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401
Db 387 KKTDTVTNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 13
US-10-473-127-1765
; Sequence 1765, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2001-03-28
; PRIOR FILING DATE: 2001-05-21
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-10-01
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1765
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1765

Query Match 100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSPDYQKTGMNDNWLKSGCQNTSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSPDYQKTGMNDNWLKSGCQNTSTK 86
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIVTHI 120
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIVTHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 206
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVLYKWDYTYANNMTFQVWLHAPL 240
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVLYKWDYTYANNMTFQVWLHAPL 266
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFQNGYVFKGIYLLRVOASDGNNTFSWSEIKEDT 300
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFQNGYVFKGIYLLRVOASDGNNTFSWSEIKEDT 326
Qy 301 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYELIIFWENTSNARKEIIE 360
Db 327 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYELIIFWENTSNARKEIIE 386
Qy 361 KKTDTVTNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401
Db 387 KKTDTVTNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 15
US-10-473-127-1772
; Sequence 1772, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
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Db 387 KKTDTVTNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 14
US-10-473-127-1766
; Sequence 1766, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2001-03-28
; PRIOR FILING DATE: 2001-05-21
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-10-01
; PRIOR FILING DATE: 2001-12-04
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1766
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1766

Query Match 100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSPDYQKTGMNDNWLKSGCQNTSTK 60
Db 27 GKNLSPQKVEVDIIDDNFILRNWRSDES VGNVTFSPDYQKTGMNDNWLKSGCQNTSTK 86
Qy 61 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIVTHI 120
Db 87 CNFSSLKLVNVEEIKLRIRAEKENTSSWYEVDSFTPPRKAQIGPPEVHLEADKAIVTHI 146
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 180
Db 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVEERENIYSRHKIYKLSPEITTYCLKVKAAL 206
Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVLYKWDYTYANNMTFQVWLHAPL 240
Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVLYKWDYTYANNMTFQVWLHAPL 266
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFQNGYVFKGIYLLRVOASDGNNTFSWSEIKEDT 300
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFQNGYVFKGIYLLRVOASDGNNTFSWSEIKEDT 326
Qy 301 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYELIIFWENTSNARKEIIE 360
Db 327 BQAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYELIIFWENTSNARKEIIE 386
Qy 361 KKTDTVTNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401
Db 387 KKTDTVTNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

RESULT 15
US-10-473-127-1772
; Sequence 1772, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
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; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1772
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1772

Query Match      100.0%; Score 2141; DB 5; Length 557;
Best Local Similarity 100.0%; Pred. NO. 4.2e-182;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GKNLKSPQKVEVDIIDNFIILNRNRSDESGVNTFFSDYQKTGMNDNWKLSGCONITSTK 60
Db      27  GKNLKSPQKVEVDIIDNFIILNRNRSDESGVNTFFSDYQKTGMNDNWKLSGCONITSTK 86

Qy      61  CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIHI 120
Db      87  CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIHI 146

Qy     121  SPGTKDSVMALDGLSTYSLLIWNSSGVBEERENIYSRHKIYKLSPETTYCLKVKAAL 180
Db     147  SPGTKDSVMALDGLSTYSLLIWNSSGVBEERENIYSRHKIYKLSPETTYCLKVKAAL 206

Qy     181  LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVQWLHAF 240
Db     207  LTSWKIGYSPVHCIKTTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVQWLHAF 266

Qy     241  KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEEKPDT 300
Db     267  KRNPGNHLYKWQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEEKPDT 326

Qy     301  EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTPTVIOQYPLIYBIIIFWNTSNAERKIE 360
Db     327  EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTPTVIOQYPLIYBIIIFWNTSNAERKIE 386

Qy     361  KKTDTVTPLNKLPLTVYCVKARAHMTDKLNKSSVFSDAVCE 401
Db     387  KKTDTVTPLNKLPLTVYCVKARAHMTDKLNKSSVFSDAVCE 427
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Search completed: January 17, 2006, 07:35:30  
Job time : 82.4456 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:19:53 ; Search time 16.2891 Seconds  
(without alignments)  
232.741 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427  
Perfect score: 2141  
Sequence: 1 GKNLKSPQKVEVDIIDNFI.....AHTWDEKLNKSSVFSDFVACE 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	8.5	542	6 US-10-131-826A-188	Sequence 188, Appl
2	180	8.4	553	6 US-10-636-716-2	Sequence 2, Appli
3	180	8.4	553	6 US-10-636-716-14	Sequence 14, Appl
4	180	8.4	553	6 US-10-636-716-16	Sequence 16, Appl
5	180	8.4	553	6 US-10-636-716-18	Sequence 18, Appl
6	180	8.4	553	6 US-10-636-716-20	Sequence 20, Appl
7	180	8.4	553	6 US-10-636-716-22	Sequence 22, Appl
8	180	8.4	553	6 US-10-636-716-24	Sequence 24, Appl
9	180	8.4	553	6 US-10-636-716-26	Sequence 26, Appl
10	180	8.4	553	6 US-10-636-716-28	Sequence 28, Appl
11	180	8.4	553	6 US-10-636-716-30	Sequence 30, Appl
12	180	8.4	553	6 US-10-636-716-32	Sequence 32, Appl
13	180	8.4	553	6 US-10-636-716-34	Sequence 34, Appl
14	180	8.4	553	6 US-10-636-716-36	Sequence 36, Appl
15	180	8.4	553	6 US-10-636-716-38	Sequence 38, Appl
16	180	8.4	553	6 US-10-636-716-40	Sequence 40, Appl
17	180	8.4	553	6 US-10-636-716-42	Sequence 42, Appl
18	180	8.4	553	6 US-10-636-716-44	Sequence 44, Appl
19	180	8.4	553	6 US-10-636-716-46	Sequence 46, Appl
20	180	8.4	553	6 US-10-636-716-48	Sequence 48, Appl
21	172.5	8.1	221	6 US-10-636-716-56	Sequence 56, Appl
22	167.5	7.8	221	6 US-10-636-716-54	Sequence 54, Appl
23	166.5	7.8	221	6 US-10-636-716-50	Sequence 50, Appl
24	166.5	7.8	384	7 US-11-075-351-12	Sequence 12, Appl
25	166.5	7.8	404	7 US-11-075-351-23	Sequence 23, Appl

26	166.5	7.8	404	7 US-11-075-351-25	Sequence 25, Appl
27	165.5	7.7	221	6 US-10-636-716-52	Sequence 52, Appl
28	163.5	7.6	221	6 US-10-636-716-60	Sequence 60, Appl
29	160.5	7.5	221	6 US-10-636-716-58	Sequence 58, Appl
30	147.5	6.9	311	6 US-10-131-826A-32	Sequence 32, Appl
31	147.5	6.9	311	6 US-10-512-214-16	Sequence 16, Appl
32	147.5	6.9	366	7 US-11-075-351-38	Sequence 38, Appl
33	147.5	6.9	374	7 US-11-075-351-42	Sequence 42, Appl
34	142	6.6	574	7 US-11-102-240-164	Sequence 164, App
35	123	5.7	522	7 US-11-184-399-8	Sequence 8, Appli
36	118	5.5	1005	7 US-11-113-424-63	Sequence 63, Appl
37	117.5	5.5	2214	7 US-11-080-991-94	Sequence 94, Appl
38	115	5.4	244	7 US-11-184-399-10	Sequence 10, Appl
39	115	5.4	473	7 US-11-165-141-23	Sequence 23, Appl
40	115	5.4	520	7 US-11-098-662-12	Sequence 12, Appl
41	115	5.4	520	7 US-11-165-141-19	Sequence 19, Appl
42	115	5.4	599	7 US-11-165-141-33	Sequence 33, Appl
43	109	5.1	203	7 US-11-165-141-4	Sequence 4, Appli
44	109	5.1	491	7 US-11-098-662-14	Sequence 14, Appl
45	109	5.1	491	7 US-11-165-141-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-10-131-826A-188  
; Sequence 188, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.



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; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lund, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-14

```

```

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy      4 LKSPQKVEVDIDNFIILRNRSDESVG-NVTFPSFDYQKTGMNDWIKLSGQCNITSTKCN 62
Db      37 LPKPANITFLSINMKNVLQWTPPEGLQGVKTYTYVQFYIYQKKWLKSECRNIRTYCD 96

Qy      63 FSSLKLNVEIKLIRIRA-EKENTSSWYEVDSFTPFRAQIQGPPEVHLEAEDKAIVIHIS 121
Db      97 LSATSDYEHQYAKVKAIWGTCCKWAESGRFPFLEQTQIGPPEVALTTDEKSI SVLT 156

Qy      122 PGTK-----DSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYK--LSPET 170
Db      157 APEKWKRNPELDPVSMQOIYSNLKNYVSLNKTGSRNRTWSQCVTN-----HTLVLTWLEPNT 212

Qy      171 TYCLKVKAALITSWKIGVSPVHCITKTVENE-----LPPPENIEVSQNYQ 218
Db      213 LYCVHVESFVGPFPRAQPSKQCAITLKQOSSBFKAKIIFWYVLP-----ISITV----- 263

Qy      219 VLKWDYTYANMTFOV-OWLHAFLEKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFKGIY 277
Db      264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDKRF 301

Qy      278 LLRQASQGNNTSFWSEIKFDTEI---QAFLLPVFNIRSLSDSFHYIYIAPKQSGNTP 334
Db      302 V-----PAEKIVNFTILNISDDSKISHQMSLLGKSDVSLND-----POPSGNLR 349

Qy      335 VIQDYPLIYEI-----IFWNTSNAERKIEKKTV--TVPNLKLPTVY 376
Db      350 PPQEEEEVKHLGYASHLMEIFCDSENTGTSFTQOESLSRTIPDPKTVIEY 401

```

```

RESULT 4
US-10-636-716-16
; Sequence 16, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:

```

```

; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lund, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-16

```

```

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy      4 LKSPQKVEVDIDNFIILRNRSDESVG-NVTFPSFDYQKTGMNDWIKLSGQCNITSTKCN 62
Db      37 LPKPANITFLSINMKNVLQWTPPEGLQGVKTYTYVQFYIYQKKWLKSECRNIRTYCD 96

Qy      63 FSSLKLNVEIKLIRIRA-EKENTSSWYEVDSFTPFRAQIQGPPEVHLEAEDKAIVIHIS 121
Db      97 LSATSDYEHQYAKVKAIWGTCCKWAESGRFPFLEQTQIGPPEVALTTDEKSI SVLT 156

Qy      122 PGTK-----DSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYK--LSPET 170
Db      157 APEKWKRNPELDPVSMQOIYSNLKNYVSLNKTGSRNRTWSQCVTN-----HTLVLTWLEPNT 212

Qy      171 TYCLKVKAALITSWKIGVSPVHCITKTVENE-----LPPPENIEVSQNYQ 218
Db      213 LYCVHVESFVGPFPRAQPSKQCAITLKQOSSBFKAKIIFWYVLP-----ISITV----- 263

Qy      219 VLKWDYTYANMTFOV-OWLHAFLEKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFKGIY 277
Db      264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDKRF 301

```

Qy 278 LLRQASDGNNTSFWSEIEKFDTEI---QAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 334  
Db 302 V----PAEKIVINFITLNSDDSKISHQDMSLLGKSDVSSLND-----POPSGNLR 349  
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVDV--TVPNLKLPLTVY 376  
Db 350 PQOESEVKHLGYASHLMEIFCDSEENTEGTSFTQOESLSRTIPPDKTVIEY 401

RESULT 5  
US-10-636-716-18  
; Sequence 18, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-10-636-716-18

Query Match 8.48; Score 180; DB 6; Length 553;  
Best Local Similarity 20.68; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIIDNFIILRNRSDESVG-NVTFSDYQKTMQMDNWIKLSCQNTITSKCN 62  
Db 37 LPKPNITFLSNKKNVLTQWTPPGLOGVKVTVTVQYFIYGQKWLKNSCRINRTYCD 96  
Qy 63 FSSLKUNVYBEIKRIRA-EKENTSSWYVDSTFPFRKAQIGPPVHLEADKAIVTHIS 121

Db 97 LSAETSDYEHQYAKVKAIMGTKCSKWAESGREYFPLETQIGPPEVALTTDEKSIYVLT 156  
Qy 122 PGTK-----DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170  
Db 157 APKWRNRPEDLPVSMQIYSNLKNVSLNTKSNRTWSOCVTN-----HTLVLTWLEPNT 212  
Qy 171 TYCLKVKAALLTSWKIGVYSPVHCITKTTVENE-----LPPPENIEVSVQONQY 218  
Db 213 LYCVHVESFVPGPPRAQPSKQKARTLKDQSSSEPKAKIIFWVYLP-----ISITV 263  
Qy 219 VLKWDYTYANMTFQV-OMLHAFILKRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQGIY 277  
Db 264 -----FLFSVMGYSIYRYIHVGKEKHPANLI-----LIYGNFEFKRFF 301  
Qy 278 LLRQASDGNNTSFWSEIEKFDTEI---QAPLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 334  
Db 302 V----PAEKIVINFITLNSDDSKISHQDMSLLGKSDVSSLND-----POPSGNLR 349  
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTVDV--TVPNLKLPLTVY 376  
Db 350 PQOESEVKHLGYASHLMEIFCDSEENTEGTSFTQOESLSRTIPPDKTVIEY 401

RESULT 6  
US-10-636-716-20  
; Sequence 20, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Farrah, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

```

; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-20

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKEVDIIDNFILRNRSDESVG-NVTFSDYQKTMGMNWKLSGCONITSTKCN 62
Db 37 LKPKANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLKSECRNINRYCD 96
Qy 63 FSSLKLVNVEIEKLIRRA-EKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHIS 121
Db 97 LSATSDEYHOYAKVAKIWTGKSKWAESGRFPFLETQIGPPEVALTTDEKSISVVL 156
Qy 122 PGTK-----DSVMWALDGLSFTYSLTIWKNSSGVEERIENIYSRHKIYK--LSPET 170
Db 157 APEKWKNPEDLPVSMQOYIYNLKNVSVLTKNSRTWSQCVTN-----HTLVLTWLEPT 212
Qy 171 TYCLKVAALTSWKIGVSPVHCITKTVE-----LPPENIEVSQNYQ 218
Db 213 LYCVHVESFPGPPRAQSEKQCARLTKDQSEBFKAKIIFWYVLP-----ISITV----- 263
Qy 219 VLKWDYTYANNTFOV-QWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFQNVFKGIY 277
Db 264 -----FLPSVMGYSIYRIYHVGEKHPANLI-----LIYGNEDKRF 301
Qy 278 LLRVQASDGNNTSFWSEIEKDTETI---QAFLLPVFNIRSLSDSFHYIYGAPKQSGNTP 334
Db 302 V-----PAEKVINFTLNISDLSKISHQDMSLLGKSDVSSLND-----PQSGNLR 349
Qy 335 VIQDYPLIYEI-----IFWNTSNAERKIIIEKKTVDV--TVPNLKPLTVY 376
Db 350 PQEIEEVKHLGYASHLMEIFCDSETEGTSFTQESLSRTIPDKTIVIEY 401

RESULT 7
US-10-636-716-22
; Sequence 22, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-22

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKEVDIIDNFILRNRSDESVG-NVTFSDYQKTMGMNWKLSGCONITSTKCN 62
Db 37 LKPKANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLKSECRNINRYCD 96
Qy 63 FSSLKLVNVEIEKLIRRA-EKENTSSWYEVDSFTPFKAQIGPPEVHLEADKAIVHIS 121
Db 97 LSATSDEYHOYAKVAKIWTGKSKWAESGRFPFLETQIGPPEVALTTDEKSISVVL 156
Qy 122 PGTK-----DSVMWALDGLSFTYSLTIWKNSSGVEERIENIYSRHKIYK--LSPET 170
Db 157 APEKWKNPEDLPVSMQOYIYNLKNVSVLTKNSRTWSQCVTN-----HTLVLTWLEPT 212
Qy 171 TYCLKVAALTSWKIGVSPVHCITKTVE-----LPPENIEVSQNYQ 218
Db 213 LYCVHVESFPGPPRAQSEKQCARLTKDQSEBFKAKIIFWYVLP-----ISITV----- 263
Qy 219 VLKWDYTYANNTFOV-QWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFQNVFKGIY 277
Db 264 -----FLPSVMGYSIYRIYHVGEKHPANLI-----LIYGNEDKRF 301
Qy 278 LLRVQASDGNNTSFWSEIEKDTETI---QAFLLPVFNIRSLSDSFHYIYGAPKQSGNTP 334
Db 302 V-----PAEKVINFTLNISDLSKISHQDMSLLGKSDVSSLND-----PQSGNLR 349
Qy 335 VIQDYPLIYEI-----IFWNTSNAERKIIIEKKTVDV--TVPNLKPLTVY 376
Db 350 PQEIEEVKHLGYASHLMEIFCDSETEGTSFTQESLSRTIPDKTIVIEY 401

RESULT 8
US-10-636-716-24
; Sequence 24, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```





```
Qy 335 VIODYPLIYEI-----IFWENTSNAERKIIIEKTKDV--TVPNLKPLTVY 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 350 PQEEREVKHGYASHLMEIFCDSEENTEGTSFTQESLSRTIPDPKTVIEY 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-636-716-28
; Sequence 28, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-28

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy 4 LKSPQKVEVDIDNNFILWRNSDESUG-NVTFPSDYOKTGMNDWIKLSCGNITSTKCN 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 37 LKPKANITFLSINMKNVLQWTPPEGLQGVKVTYTYQFYIGQKWLNFSECRNIRTYCD 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 63 FSSLKLVYEEIKLIRA-EKENTSSWYEVDSFTFPRKAQIGPPVHLEAEDKAIVIHIS 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 LSAETSDYEHQYAKVAINWGKCSKWAESGRFPFLETQIGPPEVAULTDEKSLSVILT 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 122 PGTK-----DSVMWALDGLSFTSILLIWNKSSGVEERIENIYSRHKIYK--LSPET 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 157 APEKWRNRPEDLPVSMQOIYSNLKYNVSVLNTKSNRTWSQCVTN-----HTLVLTWLBENT 212
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 171 TYCLKVKAAALLTSWKIGVYSPVHCICKTTVENE-----LPPPENIEVSVQVQNY 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 LYCVHVESFVGPGRRAQPSKQCARLKDQSSSEFKAKIIFWVYLP-----ISITV----- 263
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 219 VLKWDYTYANMTFQV-QMLHAFILKRNPNHLYKWKQIPDCENVKTKTCVFPQNVFQKIY 277
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 264 -----PLFSVMGYSIYRIHVHGKKEHPANLI-----LIYGNFEFKRFF 301
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 278 LLRVQASDGNSTFWSEIEKFDTEI-----QAFLLPPPVFNIRSLSDSFHYIYGAPKQSGNTP 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 V-----PAEKIVINFITLINISDSDSKISHQDMSLLGKSSDVSLSLND-----POPSGNLR 349
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 335 VIODYPLIYEI-----IFWENTSNAERKIIIEKTKDV--TVPNLKPLTVY 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 350 PQEEREVKHGYASHLMEIFCDSEENTEGTSFTQESLSRTIPDPKTVIEY 401
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-636-716-30
; Sequence 30, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-30
```



```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-34

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy      4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSPDYQKGMNDWIKLGGQNTSTKCN 62
Db      37 LPKPNITFLSINKMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLKSECRNIRTYCD 96
Qy      63 FSSLKLANVYEEIKLIRA-EKENTSSWYEVDSFTFPFRAQIGPPPEVHLEADKAIIVHIS 121
Db      97 LSAETSDYEHQYAKVKAIGWTKCKWAESGRFPFLEQTQIGPPEVALTTDEKSIISVLT 156
Qy      122 PGTK-----DSVMWALDGLSTYSLLIWKNSGVEERIENIYSHKIKYK--LSPET 170
Db      157 APEKWRNPEDLPVSMQOIYSLNLYNKSNTKSNRTWSQCVTN-----HTLVLTWLEPNT 212
Qy      171 TYCLKVKAALLTSWKIGVSPVHCITKTVE-----LPPPENIEVSQNYQ 218
Db      213 LYCVHVESFVCPPPRAQPSKQARTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263
Qy      219 VLKWDYTYANMTFOV-QWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
Db      264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDPKRFF 301
Qy      278 LLRVQASDGNNTSFWSSEIKEDTEI---QAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
Db      302 V-----PAEKIVINFITLNISSDKISHQDMSLLGKSSDVSLND-----POPSGNLR 349
Qy      335 VIQDYPLIYEI-----IFWNTSNAERKIIIEKTDV--TVPNLKPITY 376
Db      350 PPQEEVEKHLYGASHLMELFCDSENTGTSFTQOESLSRTIPDKTIVIEY 401

RESULT 14
US-10-636-716-36
; Sequence 36, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmborg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
```

```
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-36

Query Match      8.4%; Score 180; DB 6; Length 553;
Best Local Similarity 20.6%; Pred. No. 2.7e-08;
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;

Qy      4 LKSPQKVEVDIIDNFILRNRSDESVG-NVTFSPDYQKGMNDWIKLGGQNTSTKCN 62
Db      37 LPKPNITFLSINKMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLKSECRNIRTYCD 96
Qy      63 FSSLKLANVYEEIKLIRA-EKENTSSWYEVDSFTFPFRAQIGPPPEVHLEADKAIIVHIS 121
Db      97 LSAETSDYEHQYAKVKAIGWTKCKWAESGRFPFLEQTQIGPPEVALTTDEKSIISVLT 156
Qy      122 PGTK-----DSVMWALDGLSTYSLLIWKNSGVEERIENIYSHKIKYK--LSPET 170
Db      157 APEKWRNPEDLPVSMQOIYSLNLYNKSNTKSNRTWSQCVTN-----HTLVLTWLEPNT 212
Qy      171 TYCLKVKAALLTSWKIGVSPVHCITKTVE-----LPPPENIEVSQNYQ 218
Db      213 LYCVHVESFVCPPPRAQPSKQARTLKQSSSEFKAKIIFWYVLP-----ISITV----- 263
Qy      219 VLKWDYTYANMTFOV-QWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
Db      264 -----FLFSVMGYSIYRIHVGEKHPANLI-----LIYGNEDPKRFF 301
Qy      278 LLRVQASDGNNTSFWSSEIKEDTEI---QAFLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
Db      302 V-----PAEKIVINFITLNISSDKISHQDMSLLGKSSDVSLND-----POPSGNLR 349
Qy      335 VIQDYPLIYEI-----IFWNTSNAERKIIIEKTDV--TVPNLKPITY 376
Db      350 PPQEEVEKHLYGASHLMELFCDSENTGTSFTQOESLSRTIPDKTIVIEY 401
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Db 350 PPOEEEVKHLGYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIEY 401

RESULT 15

US-10-636-716-38  
; Sequence 38, Application US/10636716  
; Publication No. US20050244832A9  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Kho, Choon J.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Parrish, Theresa M.  
; TITLE OF INVENTION: CYTOKINE RECEPTOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/636,716  
; FILING DATE: 07-AUG-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,087  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/803,305  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lund, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-24C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 553 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-10-636-716-38

Query Match 8.4%; Score 180; DB 6; Length 553;  
Best Local Similarity 20.6%; Pred. No. 2.7e-08;  
Matches 85; Conservative 75; Mismatches 166; Indels 86; Gaps 15;  
  
Qy 4 LKSPQKEVDIIDNFI LRNRSDESG-NVTFESFDYQKGMNWKLSGCONITSTKCN 62  
Db 37 LPKPANITFISINMKNVLQWTPPEGLQGVKVTYTVQYFIYQKKWLKNSCRNIRTYCD 96  
  
Qy 63 FSSLKLANVYBEIKLIRA-EKENTSSWYEDSFTFPRKAQIGPPPEVHLEAFDKAIVIHIS 121  
Db 97 LSAETSDYEHQYAKVAKIWTCKWAESGRFYFPLETQIGPPEVALTTDEKSISVULT 156  
  
Qy 122 PGTK-----DSVMWALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYK--LSPET 170  
Db 157 APEKWKRNPDLPVSMQOIYSNLKYNVSLNLTNSRTWSQCVTN----HTLVLTWLEPNT 212

Qy 171 TYCLKVKAAALLTSWKIGVYSPVHCIKTTVENE-----LPPPENIEVSVQONY 218  
Db 213 LYCVHVESFVPGPPRAQSEKQCARTLKDOSSEFKAKIIFWVYLP-----ISITV----- 263  
  
Qy 219 VLKWDYTYANMTFQV-QWLHAFILKRNPNHLYKWKQIIPDCENVKTTQCVFPQNVFQKIY 277  
Db 264 -----FLFSVMGYSIYRYIHVGKEKHPANLI-----LIYGNEFDKRF 301  
  
Qy 278 LLRVQASDGNNTSFWSEEEKFDTETI---QAFLLPPVFNIRBSLSDSFHIYIGAPKQSGNTP 334  
Db 302 V-----PAEKIVINFITLINISDDSKISHQMSLLIGKSDVSSLND-----POPSGNLR 349  
  
Qy 335 VIQDYPLIYEI-----IFWENTSNAERKIIIEKKTDV--TVPNLKPLTVY 376  
Db 350 PPOEEEVKHLGYASHLMEIFCDSEENTEGTSFTQBSLSRTIPPDKTVIEY 401

Search completed: January 17, 2006, 07:36:15  
Job time : 17.2891 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:06:01 ; Search time 121.892 Seconds  
(without alignments)  
2523.620 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVVLGATLVLVAVGPVW.....KSSVFSDAVCEKTKPGNTSK 436

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2307	99.7	557	1	INARI1 HUMAN
2	2307	99.7	557	2	Q53H11 HUMAN
3	2300	99.4	557	2	Q53GW9 HUMAN
4	2030	87.8	387	2	Q6PKD7 HUMAN
5	1699.5	73.5	477	2	Q4R727 MACACA
6	1546	66.8	560	1	INARI1 PIG
7	1507	65.2	560	1	INARI1 BOVIN
8	1503	65.0	560	1	INARI1 SHEEP
9	1154.5	49.9	332	2	Q5GK86 SHEEP
10	1069	46.2	590	1	INARI1 MOUSE
11	1062	45.9	590	2	Q80UR8 MOUSE
12	1061	45.9	590	2	Q80UJ3 MOUSE
13	695.5	30.1	449	2	Q5XY05 CHICK
14	695.5	30.1	449	2	Q5XY05 CHICK
15	689.5	29.8	442	2	Q5PVJ9 CHICK
16	686.5	29.7	569	2	Q5YH00 CHICK
17	262.5	11.3	111	2	Q6LD20 MOUSE
18	246	10.6	98	2	Q6LD22 MOUSE
19	232	10.0	317	2	Q58CP3 BOVIN
20	228.5	9.9	325	1	110R2 HUMAN
21	222.5	9.6	327	2	Q8ZVU9 HUMAN
22	222.5	9.6	349	1	110R2 MOUSE
23	222.5	9.6	351	2	Q8VHM7 MOUSE
24	208.5	9.0	362	2	Q764M7 PIG
25	204.5	8.8	334	2	Q5RL90 CHICK
26	203	8.8	332	2	Q78EC1 CHICK
27	203	8.8	332	2	Q63953 CHICK
28	200	8.6	333	2	Q7ZT30 TETNG
29	198	8.6	553	1	120RA HUMAN
30	190	8.2	59	2	Q5GK85 SHEEP
31	189.5	8.2	341	2	Q9YGC8 CHICK

32	189	8.2	213	2	Q8C352 MOUSE	Q8C352 mus musculu
33	185.5	8.0	546	1	120RA MOUSE	Q6phb0 mus musculu
34	174	7.5	209	2	Q96SH7 HUMAN	Q96sh7 homo sapien
35	161	7.0	499	2	Q5PPL9 XENLA	Q5ppl9 xenopus lae
36	160.5	6.9	336	2	Q800E8 TETNG	Q800e8 tetraodon n
37	160.5	6.9	502	2	Q5U488 XENLA	Q5u488 xenopus lae
38	155.5	6.7	337	1	1NGR2 HUMAN	P38484 homo sapien
39	155.5	6.7	568	2	Q800F7 TETNG	Q800f7 tetraodon n
40	155.5	6.7	568	2	Q800G1 TETNG	Q800g1 tetraodon n
41	153.5	6.6	338	2	Q800G2 TETNG	Q800g2 tetraodon n
42	151	6.5	574	2	Q9HB22 HUMAN	Q9hb22 homo sapien
43	151	6.5	574	2	Q8N6P7 HUMAN	Q8n6p7 homo sapien
44	150.5	6.5	1462	2	Q612R6 CABER	Q612r6 caenorhabdi
45	147.5	6.4	311	1	120RB HUMAN	Q6ux10 homo sapien

## ALIGNMENTS

## RESULT 1

ID	INARI1 HUMAN	STANDARD;	PRT;	557 AA.
AC	P17181; Q8WTZ2;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-FEB-2005 (Rel. 46, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Interferon-alpha/beta receptor alpha chain precursor (IPN-alpha-REC).			
GN	Name=IFNAR1; Synonyms=IFNAR;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=90124632; PubMed=2153461;			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";			
RL	Cell 60:225-234(1990).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92129376; PubMed=1370833;			
RA	Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene.";			
RL	J. Biol. Chem. 267:2802-2809(1992).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-168; ILE-307 AND MET-359.			
RP	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O., Rajkumar N., Yi Q., Nickerson D.A.;			
RA	"SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-FRCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (JUN-04) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT VAL-168.			
RP	TISSUE=Brain;			
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullighan S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullighan S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RN PHOSPHORYLATION BY TYK2.  
 RX MEDLINE=95059042; PubMed=7526154;  
 RA Colamonici O., Yan H., Domanski P., Handa R., Smalley D.,  
 RA Mullersman J., Witte M., Krishnan K., Krolewski J.,  
 RT "Direct binding to and tyrosine phosphorylation of the alpha subunit  
 RT of the type I interferon receptor by p135tyk2 tyrosine kinase.";  
 RL Mol. Cell. Biol. 14:8133-8142(1994).  
 CC -I- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
 CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
 CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
 CC subunits themselves.  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -I- TISSUE SPECIFICITY: IFN receptors are present in all tissues and  
 CC even on the surface of most IFN-resistant cells.  
 CC -I- PTM: Phosphorylated on tyrosine residues by TYK2 tyrosine kinase.  
 CC -I- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -I- SIMILARITY: Contains 3 fibronectin type-III domains.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL: J03171; AAA52730.1; -; mRNA.  
 DR EMBL: X60459; CAA42992.1; -; Genomic DNA.  
 DR EMBL: AV654286; AAT49100.1; -; Genomic DNA.  
 DR EMBL: BC021825; AAH21825.1; -; mRNA.  
 DR F01: A32694; A32694.  
 DR Ensembl: ENSG00000142166; Homo sapiens.  
 DR HGNC: HGNC:5432; IFNAR1.  
 DR H-InvDB: HIX0016075; -.  
 DR MIM: 107450; -.  
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO: GO:0004905; F:interferon-alpha/beta receptor activity; TAS.  
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 DR GO: GO:0007259; P:JAK-STAT cascade; TAS.  
 DR GO: GO:0009615; P:response to virus; TAS.  
 DR InterPro: IPR000282; Cytok receptor\_2.  
 DR InterPro: IPR003961; FN\_III.  
 DR PROSITE: PS00853; FN3; FALSE\_NEG.  
 KW Glycoprotein; Phosphorylation; Polymorphism; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 27 Potential.  
 FT CHAIN 28 557 Interferon-alpha/beta receptor alpha  
 FT TOPO\_DOM 28 436 Extracellular (Potential).  
 FT TRANSMEM 437 457 Potential.  
 FT TOPO\_DOM 458 557 Cytoplasmic (Potential).  
 FT DOMAIN 134 224 Fibronectin type-III 1.  
 FT DOMAIN 230 326 Fibronectin type-III 2.  
 FT DOMAIN 334 425 Fibronectin type-III 3.  
 FT MOD\_RES 466 466 Phosphotyrosine (by TYK2) (Probable).  
 FT MOD\_RES 481 481 Phosphotyrosine (by TYK2) (Probable).  
 FT CARBOHYD 50 50 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 58 58 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 81 81 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 314 314 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 416 416 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 433 433 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 79 87 By similarity.

FT DISULFID 199 220 By similarity.  
 FT VARIANT 168 168 L -> V.  
 FT VARIANT 307 307 /FTId=VAR\_002717.  
 FT VARIANT 359 359 V -> I.  
 FT VARIANT 359 359 /FTId=VAR\_020502.  
 FT CONFLICT 17 17 T -> M.  
 FT CONFLICT 17 17 /FTId=VAR\_020503.  
 FT SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75CBC CRC64;  
 SQ  
 Query Match 99.7%; Score 2307; DB 1; Length 557;  
 Best Local Similarity 99.8%; Pred. No. 3.1e-166;  
 Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MMVLLGATTLVLVAVGPWLSAAAGKNLKSPOKVEVDIIDNFTLRNRSDESVCNVT 60  
 DB 1 MMVLLGATTLVLVAVGPWLSAAAGKNLKSPOKVEVDIIDNFTLRNRSDESVCNVT 60  
 QY 61 FSPDYQKTGMNDWIKLSGCGNITSTKCNFSSLLKLVYEEIKLRIRAEKENTSSWYVDSF 120  
 DB 61 FSPDYQKTGMNDWIKLSGCGNITSTKCNFSSLLKLVYEEIKLRIRAEKENTSSWYVDSF 120  
 QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLIWNKSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSFTYSLIWNKSSGVEERI 180  
 QY 181 ENIYSHKIKLSPETTYCLKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
 DB 181 ENIYSHKIKLSPETTYCLKVAALLTSWKIGVSPVHCITTVENELPPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVQWLHAFILKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
 DB 241 NQNYVLKWDYTYANMTFQVQWLHAFILKRNPGNHLKWKQIPDCENVKTTQCVPQNVFQK 300  
 QY 301 GYLLRVQASDGNNTSFWSSEIKFDTETIQAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 DB 301 GYLLRVQASDGNNTSFWSSEIKFDTETIQAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 QY 361 VTQDPLIYEIIFWNTSNAERKIEKKTDTVFNKLPLTVYCVKARAHTMDEKLNKSSV 420  
 DB 361 VTQDPLIYEIIFWNTSNAERKIEKKTDTVFNKLPLTVYCVKARAHTMDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 DB 421 FSDAVCEKTKPGNTSK 436  
 RESULT 2  
 Q53H11 HUMAN  
 ID Q53H11\_HUMAN PRELIMINARY; PRT; 557 AA.  
 AC Q53H11\_HUMAN PRELIMINARY; PRT; 557 AA.  
 DT 13-SEP-2005 (TRENBLrel. 31, Created)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE Interferon-alpha receptor 1 variant (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Maruyama K., Sugano S.;  
 RT "Oligo-capping: a simple method to replace the cap structure of  
 RT eucaryotic mRNAs with oligoribonucleotides.";  
 RL Gene 138:171-174(1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;  
 RT "Construction and characterization of a full length-enriched and a 5'-  
 RT end-enriched cDNA library.";

```

RT      Gene 200:149-156 (1997).
RT      [3]
RT      end-enriched cDNA library.
RL      Gene 200:149-156 (1997).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Liver;
RA      Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA      Tanaka A., Yokoyama S.;
RA      Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AK222770; BAD96490.1; -, mRNA.
KW      Receptor.
FT      NON TER
SQ      SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75CBC CRC64;

Query Match      99.7%; Score 2307; DB 2; Length 557;
Best Local Similarity 99.8%; Pred. No. 3.1e-166;
Matches 435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60
Db      1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60

Qy      61 FSPDYQKTGMNDNWKLSGCONITSTKCNFSSKLNVYEEIKLIRAEKENTSSWYVDSF 120
Db      61 FSPDYQKTGMNDNWKLSGCONITSTKCNFSSKLNVYEEIKLIRAEKENTSSWYVDSF 120

Qy      121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEERI 180
Db      121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEERI 180

Qy      181 ENIYSRHKIYKLPETTYCLVKAAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240
Db      181 ENIYSRHKIYKLPETTYCLVKAAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240

Qy      241 NQNVLLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNFQK 300
Db      241 NQNVLLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNFQK 300

Qy      301 GIYLLRVOASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360
Db      301 GIYLLRVOASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360

Qy      361 VIQDYPLIYEIIFWENTSNARKEIIKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
Db      361 VIQDYPLIYEIIFWENTSNARKEIIKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420

Qy      421 PSDAVCEKTKPGNTSK 436
Db      421 PSDAVCEKTKPGNTSK 436

RESULT 3
Q53GW9 HUMAN PRELIMINARY; PRT; 557 AA.
AC      Q53GW9;
DT      13-SEP-2005 (TrEMBLrel. 31, Created)
DT      13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE      Interferon-alpha receptor 1, variant (fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Liver;
RA      Maruyama K., Sugano S.;
RT      "Oligo-capping: a simple method to replace the cap structure of
RT      eucaryotic mRNAs with oligoribonucleotides.";
RL      Gene 138:171-174 (1994).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Liver;
RA      Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;

*Construction and characterization of a full length-enriched and a 5'-
end-enriched cDNA library.*;
Gene 200:149-156 (1997).
[3]
NUCLEOTIDE SEQUENCE.
TISSUE=Liver;
Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
Tanaka A., Yokoyama S.;
Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
EMBL; AK222812; BAD96532.1; -, mRNA.
Receptor.
NON TER
SEQUENCE 557 AA; 63598 MW; 2D9522BECC775486 CRC64;

Query Match      99.4%; Score 2300; DB 2; Length 557;
Best Local Similarity 99.3%; Pred. No. 1e-165;
Matches 433; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60
Db      1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFILRNRSDESNGVT 60

Qy      61 FSPDYQKTGMNDNWKLSGCONITSTKCNFSSKLNVYEEIKLIRAEKENTSSWYVDSF 120
Db      61 FSPDYQKTGMNDNWKLSGCONITSTKCNFSSKLNVYEEIKLIRAEKENTSSWYVDSF 120

Qy      121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEERI 180
Db      121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWNKSSGVVEERI 180

Qy      181 ENIYSRHKIYKLPETTYCLVKAAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240
Db      181 ENIYSRHKIYKLPETTYCLVKAAALTSWKIGYSPVHCITKTVENELPPENIEVSQ 240

Qy      241 NQNVLLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNFQK 300
Db      241 NQNVLLKWDYTYANMTFQVQWLHAFKRNPNHLYKWKQIPDCENVKTTQCVFPQNFQK 300

Qy      301 GIYLLRVOASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360
Db      301 GIYLLRVOASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLDSFHYIYGAPQSGNTP 360

Qy      361 VIQDYPLIYEIIFWENTSNARKEIIKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
Db      361 VIQDYPLIYEIIFWENTSNARKEIIKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420

Qy      421 PSDAVCEKTKPGNTSK 436
Db      421 PSDAVCEKTKPGNTSK 436

RESULT 4
Q6PKD7 HUMAN PRELIMINARY; PRT; 387 AA.
AC      Q6PKD7;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE      Interferon-alpha receptor 1 variant (fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Ovary;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smillius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002590; AAH02590.1; -: mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro: IPR000282; Cytok_receptor_2.
FT NON TER 387
SQ SEQUENCE 387 AA; 44388 MW; DEC1A8CC2F44499 CRC64;

Query Match 87.8%; Score 2030; DB 2; Length 387;
Best Local Similarity 99.5%; Pred. No. 1.9e-145;
Matches 381; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMVVLGATTLVLVAVGPVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGNVT 60
DB 1 MMVVLGATTLVLVAVAPVLSAAAGGNLKSQKVEVDIIDNFILRNRSDESNGNVT 60

QY 61 FSPDYQKTGMNDIKLSGCCQNTSTKCNFSLKLVYEEIKLIRAEKENTSSWYEDSF 120
DB 61 FSPDYQKTGMNDIKLSGCCQNTSTKCNFSLKLVYEEIKLIRAEKENTSSWYEDSF 120

QY 121 TPRFKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMALDGLSTYSLLIWNSSGVEERI 180
DB 121 TPRFKAQIGPPEVHLEAEDKAIIVHISPGTKDSVMALDGLSTYSLLIWNSSGVEERI 180

QY 181 ENIYSRHKIYKLPETTYCLKVKAAALTSWKIGVYSPVHCITKTVENELPPPNIEVSQ 240
DB 181 ENIYSRHKIYKLPETTYCLKVKAAALTSWKIGVYSPVHCITKTVENELPPPNIEVSQ 240

QY 241 NQNVYLKWDYTYANMTFQVQWLHAFKRPNFNGHLYKWKQIPDCENVKTTQCVPFQNVFQK 300
DB 241 NQNVYLKWDYTYANMTFQVQWLHAFKRPNFNGHLYKWKQIPDCENVKTTQCVPFQNVFQK 300

QY 301 GIYLLRVQASDGNNTSFWSEIEIKFDTIEQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360
DB 301 GIYLLRVQASDGNNTSFWSEIEIKFDTIEQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

QY 361 VIQDYPLIYELIIFWENTSNARK 383
DB 361 VIQDYPLIYELIIFWENTSNARK 383

RESULT 5
Q4R727 MACFA
ID Q4R727_MACFA PRELIMINARY; PRT; 477 AA.
AC Q4R727;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Testis cDNA, clone: Q4R727-16508, similar to human interferon (alpha,
DE beta and omega) receptor 1 (IFNAR1), mRNA, RefSeq: NM_000629.2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
[1] NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA International consortium for macaque cDNA sequencing, analysis;
RT "DNA sequences of macaque genes expressed in brain or testis and its
RT evolutionary implications.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Oeada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT "Substitution rate and structural divergence of 5'UTR evolution:
RT Comparative analysis between human and cynomolgus monkey cDNAs.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL: AB169002; BAB01097.1; -: mRNA.
DR InterPro: IPR000282; Cytok_receptor_2.
KW Receptor; Transmembrane.
SQ SEQUENCE 477 AA; 54766 MW; 1D4110D471060BCF CRC64;

Query Match 73.5%; Score 1699.5; DB 2; Length 477;
Best Local Similarity 90.7%; Pred. No. 2.9e-120;
Matches 323; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 82 ITSTKCNFSSKLNVYEEIKLIRAEKENTSSWYEDSFPPFKAQIGPPEVHLEAEDKA 141
DB 1 MSTKCNFSSKLNVYDEIKLIRAEKENTSSWCEVDSFPFKAQIGPPEVHLEAEDKA 60

QY 142 IVIHIS-PGTQDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLPETTYCL 200
DB 61 IVIYISPPGTDSVMALDRSSFTYSLIWNSSSVEERIENIYSRHKIYKLPETTYCL 120

QY 201 KVKAAALTSWKIGVYSPVHCITKTVENELPPPNIEVSQNVYKWDYTYANMTFQVQ 260
DB 121 KVKAAALTSRKIGVYSPVHCITKTVENELPPPNIEVIVQNVYKWDYTYANMTFQVQ 180

QY 261 WLHAFKRPNFNGHLYKWKQIPDCENVKTTQCVPFQNVFQKGIYLLRVQASDGNNTSFWSE 320
DB 181 WLHAFKRPNFNGHLYKWKQIPDCENVKTTQCVPFQNVFQKGIYLLRVQASDGNNTSFWSE 240

QY 321 EIKFDTIEQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPVIQDYPLIYELIIFWENTSN 380
DB 241 EIKFDTIEQAFLLPPVFNIRSLSDSLHSIGAPKSENKPVQDYPLIYELIIFWENTSKA 300

QY 381 ERKIETKTDVTVPNLKPLTVYCVKRAHMTDEKLNKSSVFSFSDAVCEKTPGNTSK 436
DB 301 ERKIETKTDVTVPNLKPLTVYCVKRAHSMDEKLNKSSVFSFSDVWCEETKSGNTSK 356

RESULT 6
INAR1_PIG
ID INAR1_PIG STANDARD; PRT; 560 AA.
AC Q764M8;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interferon-alpha/beta receptor alpha chain precursor (1FN-alpha-REC).
GN Name=IFNARI;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=14681463; DOI=10.1093/nar/gkh037;
RA Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H.,
RA Okumura N., Hamasima N., Awata T.;
RT "PEDE (Pig EST Data Explorer): construction of a database for ESTs
RT derived from porcine full-length cDNA libraries.";
RL Nucleic Acids Res. 32:D484-D488 (2004).
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type

```



I IFNs triggers tyrosine phosphorylation of a number of proteins including JAKs, TYK2, STAT proteins and IFN $\alpha$  and beta-subunits themselves (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Belongs to the type II cytokine receptor family.

-!- SIMILARITY: Contains 3 fibronectin type-III domains.

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EMBL; AB116561; BAD06315.1; -; mRNA.  
 InterPro; IPR000282; Cytok receptor\_2.  
 InterPro; IPR003961; FN III.  
 PROSITE; PS0853; FN3; FALSE NEG.  
 Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 SIGNAL 1 24 By similarity.  
 CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.

TOPO\_DOM 25 437 Extracellular (Potential).  
 TRANSMEM 438 458 Potential.  
 TOPO\_DOM 459 560 Cytoplasmic (Potential).  
 DOMAIN 133 224 Fibronectin type-III 1.  
 DOMAIN 230 326 Fibronectin type-III 2.  
 DOMAIN 334 426 Fibronectin type-III 3.  
 CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 222 222 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 417 417 N-linked (GlcNAc...) (Potential).  
 DISULFID 76 84 By similarity.  
 FT DISULFID 199 220 By similarity.  
 SQ SEQUENCE 560 AA; 63221 MW; DC193651033DFBDB CRC64;

Query Match 66.8%; Score 1546; DB 1; Length 560;  
 Best Local Similarity 66.7%; Pred. No. 1.5e-108;  
 Matches 293; Conservative 67; Mismatches 73; Indels 6; Gaps 5;

2 MVVLGATTLVLVAVGPMVLAAAGKVLKSPQKVEVDIIDDNFILRNWRSDESGVNTF 61  
 1 MGLGLGATTLMLVAGAPVL--PAGGADLRSPENVVSIIDDNFILRWKSSSVNTF 58  
 62 SFYQKQGMNDWIKLSCGQNTITKCNFSSLLK-NVYEEIKLIRAEKEN-TSSWYEYDS 119  
 59 SADYQITGMNDWIKLPGQYVTSFECNFSSIKLSKVYEKTLIRAEKGNSTSPWYVEP 118  
 120 FTFPRKQIGPPEVHLEADKAIVHIS-PGKDSVMWALDGLFTYSLLIWKNSGVVEE 178  
 119 FIPFQEAIGPDPVHLEADKAIINTLSPPTKNSVMWAMSSSFVYSLVTKNSSSLE 178  
 179 RIENYSRHKYKLSPEYTKVKAALLTSWKGIVSPVHCITVTYENELPPENLEVS 238  
 179 RKTGYARDKIHQSPETTYCLKVKAGLRSPKGVSPVYCINTVVKHLPSPENLEIN 238  
 239 VQNGYVLKWDYTYANMTFQVQLHAFILKRNPGNHLKWKQIPCCENVKTTQCVPQNVF 298  
 239 AENRYVLKWNYYENVTFQQLHAFILKLPEDHSDKWKQIPCCENVKTTCTHCVFQNVF 298  
 299 QKGYLLRVQASDGNSTSWSEEEKFDEIQAFLLPPVFNTRISLD-SFHYIGAPKQSG 357  
 299 TKGIFIRVQASDGNSTSLWSEERKFNTEMQTLFPPVNNKPNINDASLRVIGAPKESE 358  
 358 NTPVIQDPLIYEIFWENTNABRKIIKKTDTVPLKPLTYCVKARHTWDEKLK 417  
 359 DKSQNLQPLIYEIVFENTSDTERDVLKRTDFTFSLNKLPLTYCVKARALIENDRNR 418

Qy 418 SSVFSDAVCEKTKPGNTSK 436  
 Db 419 SSVFSDVCEKTKPGSTSQ 437

RESULT 7  
 INARI\_BOVIN  
 ID INARI\_BOVIN STANDARD; PRT; 560 AA.  
 AC Q04790;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
 GN Name=IFNARI; Synonyms=IFNAR;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Theria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MIMLINE=93076908; PubMed=1446745; DOI=10.1016/0014-5793(92)81204-Y;  
 RA Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;  
 RT "Specific antiviral activities of the human alpha interferons are determined at the level of receptor (IFNAR) structure."  
 RL FEBS Lett. 313:255-259(1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MIMLINE=93305725; PubMed=8318540; DOI=10.1016/0167-4781(93)90129-2;  
 RA Lim J.-K., Langer J.A.;  
 RT "Cloning and characterization of a bovine alpha interferon receptor."  
 RL Biochim. Biophys. Acta 1173:314-319(1993).  
 CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type I IFNs triggers tyrosine phosphorylation of a number of proteins including JAKs, TYK2, STAT proteins and IFN $\alpha$  and beta-subunits themselves.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.

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EMBL; X68443; CAA48484.1; -; mRNA.  
 EMBL; L08320; AAA02571.1; -; mRNA.  
 PIR; S27387; S27387.  
 InterPro; IPR000282; Cytok receptor\_2.  
 InterPro; IPR003961; FN III.  
 InterPro; IPR001187; Tissue factor.  
 Pfam; PF01108; Tissue\_fac; 1.  
 DR PROSITE; PS0853; FN3; 2.  
 DR Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 SIGNAL 1 24 By similarity.  
 CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.  
 TOPO\_DOM 25 437 Extracellular (Potential).  
 TRANSMEM 438 458 Potential.  
 TOPO\_DOM 459 560 Cytoplasmic (Potential).  
 DOMAIN 133 224 Fibronectin type-III 1.  
 DOMAIN 230 326 Fibronectin type-III 2.  
 DOMAIN 334 426 Fibronectin type-III 3.  
 CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).

```
FT CARBOHYD 434 434 N-linked (GlcNAc... ) (Potential).
FT DISULFID 76 84 By similarity.
FT DISULFID 199 220 By similarity.
FT CONFLICT 422 422 F -> V (in Ref. 2).
SQ SEQUENCE 560 AA; 63918 MW; 66D76B72861E1D11 CRC64;

Query Match
Best Local Similarity 64.9%; DB 1; Length 560;
Matches 285; Conservative 65; Mismatches 83; Indels 6; Gaps 6;

QY 2 MVLGATTLVLVAVGPWVLSAAGCKNLKSPQKVEVDIIDDNFILWNRSDSVGNVTF 61
Db 1 MLALLGATTLMLVA-GRWVLPASGEANLK-PENVEIHIIDDNFFLKNSSSSVKNVTF 58

QY 62 SFDYQKTMNDWIKLSGCONITSTKCNFSSLLK-NVYEIKLRIRAEK-ENTSSWYEVDS 119
Db SADYQILGTDNWKLLPGCOHITSSKCNFSSVELKDVFEKIELIRAEKGNNTWTWEVEP 118

QY 120 FTFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMWALDGLSFTYSLLIWKNSSGVVE 178
Db FVFPLEAQIGPPDVHLEAEDKAIILSPGPTEDSIMWALDRSSFRYSVVIWKNSSLEE 178

QY 179 RIENIYSRHKIYKLSPEITTYCLVKVAALLTSWKIGVSPVHCITKTVENELPPENIEVS 238
Db RIETVPEDKIYKLSPEITTYCLVKVAELRLQSRVGCYSPVYCINTTTERHKVSPENIQIN 238

QY 239 VQONQYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTKQCVPQNVF 298
Db ADNQIYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVTSTHCVFPEVS 298

QY 299 QKGIYLLRVOASDGNNTFSWSEIKFDTETQAFLLPVPFNIRLS-DSFHYIYCAPKQSG 357
Db SRGIYVVRVRAASNGSGTSFWSEKEFNTKTIIFPPVIVSKVSDTDLHVSVGASESE 358

QY 358 NTPVIQDYPILYLIFFWNTSNARKEIIEKTDVTVPNLKPLTYCVKARAHMTDEKLNK 417
Db NMSVNLQYPLIYEVIFWNTSNARKEVLEKRTNFIIPDLKPLTYCVKARALIENDRRNK 418

QY 418 SSVFSDAVCEKTPGNTSK 436
Db GSSFSDVCEKTPGNTSK 437

RESULT 8
ID INARI SHEEP STANDARD; PRT; 560 AA.
AC Q28589; Q95206;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)
DE (Interferon alpha/beta receptor-1).
GN Name=IFNAR1; Synonyms=IFNAR;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Endometrium;
RX MEDLINE=97135690; PubMed=8981227; DOI=10.1677/jme.0.0170207;
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in
endometrium.";
RL J. Mol. Endocrinol. 17:207-215(1996).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Endometrium;
RX MEDLINE=98006426; PubMed=9348203; DOI=10.1210/en.138.11.4757;
RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
subunits from uteri, and endometrial expression of messenger
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RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy.";
RL Endocrinology 138:4757-4767(1997).
CC -I- FUNCTION: Receptor for interferons alpha and beta. Binding to type
CC I IFNs triggers tyrosine phosphorylation of a number of proteins
CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-
CC subunits themselves.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: Expressed in all tissues examined except
CC conceptus at day 15 of pregnancy.
CC -I- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -I- SIMILARITY: Contains 3 fibronectin type-III domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X95939; CAA65183.1; -, mRNA.
CC EMBL; U65978; AAB84231.1; -, mRNA.
CC InterPro; IPR002822; Cytok_receptor_2.
CC InterPro; IPR003961; FN_III.
CC PROSITE; P850853; FN3; 3.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 560 Interferon-alpha/beta receptor alpha
FT chain.
FT TOPO_DOM 25 437 Extracellular (Potential).
FT TRANSMEM 438 458 Potential.
FT TOPO_DOM 459 560 Cytoplasmic (Potential).
FT DOMAIN 125 224 Fibronectin type-III 1.
FT DOMAIN 230 326 Fibronectin type-III 2.
FT DOMAIN 330 426 Fibronectin type-III 3.
FT CARBOHYD 47 47 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 55 55 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 85 85 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 108 108 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 222 222 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 313 313 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 359 359 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 377 377 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 434 434 N-linked (GlcNAc... ) (Potential).
FT DISULFID 76 84 By similarity.
FT DISULFID 199 220 By similarity.
FT CONFLICT 352 352 S -> G (in Ref. 2).
FT CONFLICT 522 522 A -> D (in Ref. 2).
SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

Query Match 65.0%; Score 1503; DB 1; Length 560;
Best Local Similarity 64.5%; DB 1; Length 560;
Matches 283; Conservative 68; Mismatches 82; Indels 6; Gaps 6;

QY 2 MVLGATTLVLVAVGPWVLSAAGCKNLKSPQKVEVDIIDDNFILWNRSDSVGNVTF 61
Db 1 MVLGATTLMLVA-GRWVLPASGEANLK-ENVEIHIIDDNFFLKNSSSSVKNVTF 58

QY 62 SFDYQKTMNDWIKLSGCONITSTKCNFSSLLK-NVYEIKLRIRAEK-ENTSSWYEVDS 119
Db SADYQILGTDNWKLLPGCOHITSSKCNFSSVELKDVFEKIELIRAEKGNNTWTWEVEP 118

QY 120 FTFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMWALDGLSFTYSLLIWKNSSGVVE 178
Db FVFPLEAQIGPPDVHLEAEDKAIILSPGPTEDSIMWALDRSSFRYSVVIWKNSSLEE 178

QY 179 RIENIYSRHKIYKLSPEITTYCLVKVAALLTSWKIGVSPVHCITKTVENELPPENIEVS 238
Db RIETVPEDKIYKLSPEITTYCLVKVAELRLQSRVGCYSPVYCINTTTERHKVSPENIQIN 238

QY 239 VQONQYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTKQCVPQNVF 298
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Db 239 VDNQAYVLKWDYESTTFOAQLRAFLKIPGKHSNWKQIPNCENVTTHCVFPRDIF 298
Qy 299 QKGIYLLRVQASDGNNTSFWSSEIKFDTETEOAFL 332
Db 299 SMGIYVVRVRSNGNGTSFWSSEKEFTEVKLF 332
Qy 358 NTPVIQDPIYLIIFWNTSNAERKLEKTDVTVPNLKPLTYCVKARAHMTDEKLNK 417
Db 359 NMSYNQYLPYVIFWNTSNAERKLEKTDVTVPNLKPLTYCVKARALINDRWNK 418
Qy 418 SSVFSDAVCEKTKGNTSK 436
Db 419 GSSVSDTVCEKTKGNTSK 437

RESULT 9
Q9GK86_SHEEP PRELIMINARY; PRT; 332 AA.
AC Q9GK86;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type I interferon receptor 1e.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21267382; PubMed=11344274; DOI=10.1073/pnas.111139598;
RA Han C.S., Chen Y., Ezashi T., Roberts R.M.;
RT "Antiviral activities of the soluble extracellular domains of type I
interferon receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:6138-6143 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
high-frequency rearrangements in the interferon-resistant L1210 cell
line."
RL Gene 148:343-346 (1994).
CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type
I IFNs triggers tyrosine phosphorylation of a number of proteins
including JAKs, TYK2, STAT proteins and IFN alpha- and beta-
subunits themselves.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; M89641; AAA37890.1; -; mRNA.
DR PIR; A45283; A45283.
DR Ensembl; ENSMUSG0000022967; Mus musculus.
DR MGI; MGI:107658; Ifnar1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN III.
DR PROSITE; PS50853; FN3; FALSE NEG.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 590 Interferon-alpha/beta receptor alpha
chain.
FT TOPO_DOM 27 429 Extracellular (Potential).
FT TRANSMEM 430 449 Potential.
FT TOPO_DOM 450 590 Cytoplasmic (Potential).
FT DOMAIN 134 224 Fibronectin type-III 1.
FT DOMAIN 230 327 Fibronectin type-III 2.
FT DOMAIN 335 418 Fibronectin type-III 3.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 214 214 N-linked (GlcNAc...) (Potential).
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Db 239 VDNQAYVLKWDYESTTFOAQLRAFLKIPGKHSNWKQIPNCENVTTHCVFPRDIF 298
Qy 299 QKGIYLLRVQASDGNNTSFWSSEIKFDTETEOAFL 332
Db 299 SMGIYVVRVRSNGNGTSFWSSEKEFTEVKLF 332
Qy 358 NTPVIQDPIYLIIFWNTSNAERKLEKTDVTVPNLKPLTYCVKARAHMTDEKLNK 417
Db 359 NMSYNQYLPYVIFWNTSNAERKLEKTDVTVPNLKPLTYCVKARALINDRWNK 418
Qy 418 SSVFSDAVCEKTKGNTSK 436
Db 419 GSSVSDTVCEKTKGNTSK 437

RESULT 10
ID INARI_MOUSE STANDARD; PRT; 590 AA.
AC P33896;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
GN Name=ifnar1; Synonyms=ifar, ifnar;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92262522; PubMed=1533935;
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
RT "Behavior of a cloned murine interferon alpha/beta receptor expressed
in homospesific or heterospesific background."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778 (1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
high-frequency rearrangements in the interferon-resistant L1210 cell
line."
RL Gene 148:343-346 (1994).
CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type
I IFNs triggers tyrosine phosphorylation of a number of proteins
including JAKs, TYK2, STAT proteins and IFN alpha- and beta-
subunits themselves.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.
CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; M89641; AAA37890.1; -; mRNA.
DR PIR; A45283; A45283.
DR Ensembl; ENSMUSG0000022967; Mus musculus.
DR MGI; MGI:107658; Ifnar1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN III.
DR PROSITE; PS50853; FN3; FALSE NEG.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 590 Interferon-alpha/beta receptor alpha
chain.
FT TOPO_DOM 27 429 Extracellular (Potential).
FT TRANSMEM 430 449 Potential.
FT TOPO_DOM 450 590 Cytoplasmic (Potential).
FT DOMAIN 134 224 Fibronectin type-III 1.
FT DOMAIN 230 327 Fibronectin type-III 2.
FT DOMAIN 335 418 Fibronectin type-III 3.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 214 214 N-linked (GlcNAc...) (Potential).
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FT CARBOHYD 314 314 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 370 370 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 409 409 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 413 413 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 78 86 By similarity.
FT DISULFID 199 220 By similarity.
SQ SEQUENCE 590 AA; 65777 MW; 7EC6DFF370185D3A CRC64;

Query Match 46.2%; Score 1069; DB 1; Length 590;
Best Local Similarity 48.6%; Pred. No. 2.4e-72;
Matches 212; Conservative 77; Mismatches 137; Indels 10; Gaps 4;

QY 2 MVVLGATTLLVAVGPPWVLSAAGGNKLSKPKQKVEVDIIDDNFILRNWRSDES VGNVTF 61
DB 1 MLAVVGAALVLVAGAPWVLPSPAAGGNLKPENIDVYIIDNNTLKWSSHGSGSVTF 60
QY 62 SFDYQKTMGNWIKLSGCONITSTKCNFSSKLNVYEEIKLIRAEKEN-TSSWYVDSP 120
DB 61 SAEYRTKDEAKWLKVPCEQHTTTKCFSLDNTNVIKTQFRVRAEGNSTSSWNEVDPF 120
QY 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERI 180
DB 121 IPFYTAHMSPEVLEAEDKAILVHISPPGQGNWMALEKPSFYTIIRIWKSSSDKTTI 180
QY 181 ENIYSRHKIYKLPETTYCLVKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240
DB 181 NSTYVVEKIPPELLPETTYCLEVKAHPSLKKHNSYSTVQICISTTVANKMPVGNLQVDAQ 240
QY 241 NQNVLVKWDY-TYANMTFOVQMLHAFKRNPGNHLKWKQIIPDCENVKTKTCVFPQNVFQ 299
DB 241 GKSIVLVKWDYIASADVLFRACQMLPGYSKSSGSHDKWKPIPTCANVQTHCVFSQDVTY 300
QY 300 KGIYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKSGNT 359
DB 301 TGTFHLLVQASDGNNTSFWSEEEKFIDSKHIIIPSPVITVTWMSDILLVYVNCQDSTCD- 359
QY 360 PVIQDYPLIYEIIFWENTSNAERKIEKKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSS 419
DB 360 -----GLNVEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQARV-LFRALLNKTS 412
QY 420 VFSDAVCEKTKPGNTS 435
DB 413 NFSEKLCCKTRPGSFS 428

RESULT 11
Q80UR8_MOUSE PRELIMINARY; PRT; 590 AA.
AC Q80UR8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interferon (Alpha and beta) receptor 1.
GN Name=Ifnar1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv x 129/Sv-CP; TISSUE=ES Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Mariani K., Moore A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Mardina K., Farmer A.A., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv x 129/Sv-CP; TISSUE=ES Cell;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL; BC052217; AAHS2217.1; -; mRNA.
DR MGI; MGI:107658; Ifnar1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000282; Cytok receptor_2.
DR InterPro; IPR003961; FN_III.
DR SMART; SM00060; FN3; 3.
DR Receptor; Transmembrane.
KW Receptor; Transmembrane.
SQ SEQUENCE 590 AA; 65713 MW; E8383FFA6BE3AF3C CRC64;

Query Match 45.9%; Score 1062; DB 2; Length 590;
Best Local Similarity 48.4%; Pred. No. 8.2e-72;
Matches 211; Conservative 77; Mismatches 138; Indels 10; Gaps 4;

QY 2 MVVLGATTLLVAVGPPWVLSAAGGNKLSKPKQKVEVDIIDDNFILRNWRSDES VGNVTF 61
DB 1 MLAVVGAALVLVAGAPWVLPSPAAGGNLKPENIDVYIIDNNTLKWSSHGSGSVTF 60
QY 62 SFDYQKTMGNWIKLSGCONITSTKCNFSSKLNVYEEIKLIRAEKEN-TSSWYVDSP 120
DB 61 SAEYRTKDEAKWLKVPCEQHTTTKCFSLDNTNVIKTQFRVRAEGNSTSSWNEVDPF 120
QY 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGSGVEERI 180
DB 121 IPFYTAHMSPEVLEAEDKAILVHISPPGQGNWMALEKPSFYTIIRIWKSSSDKTTI 180
QY 181 ENIYSRHKIYKLPETTYCLVKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240
DB 181 NSTYVVEKIPPELLPETTYCLEVKAHPSLKKHNSYSTVQICISTTVANKMPVGNLQVDAQ 240
QY 241 NQNVLVKWDY-TYANMTFOVQMLHAFKRNPGNHLKWKQIIPDCENVKTKTCVFPQNVFQ 299
DB 241 GKSIVLVKWDYIASADVLFRACQMLPGYSKSSGSHDKWKPIPTCANVQTHCVFSQDVTY 300
QY 300 KGIYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSPHIYIGAPKSGNT 359
DB 301 TGTFHLLVQASDGNNTSFWSEEEKFIDSKHIIIPSPVITVTWMSDILLVYVNCQDSTCD- 359
QY 360 PVIQDYPLIYEIIFWENTSNAERKIEKKTDTVTVPNLKPLTVYCVKARAHTMDKLNKSS 419
DB 360 -----GLNVEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQARV-LFRALLNKTS 412
QY 420 VFSDAVCEKTKPGNTS 435
DB 413 NFSEKLCCKTRPGSFS 428

RESULT 12
Q80UJ3_MOUSE PRELIMINARY; PRT; 590 AA.
ID Q80UJ3_MOUSE PRELIMINARY;
AC Q80UJ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Ifnar1 protein (Interferon (Alpha and beta) receptor 1).
GN Name=Ifnar1;
OS Mus musculus (Mouse).

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Qy 409 HTWDEKLNKSSVFSDDAVCEKTKPG 432
Db 422 --FSEAYNKSSDFSRECEIGTAGG 443

RESULT 14
Q5XPII_CHICK
ID Q5XPII_CHICK PRELIMINARY; PRT; 569 AA.
AC Q5XPII;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Interferon receptor.
GN Name=IFNAR1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Han C.-L., Wang M., Gao F., Wu Z.-G.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY744159; AAU93528.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR00282; Cytok receptor_2.
DR InterPro; IPR003961; FN_III.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS50853; FN3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS50853; FN3; 4.
KW Receptor.
SQ SEQUENCE 569 AA; 64093 MW; ABC89111A5476BFB CRC64;

Query Match 30.1%; Score 695.5; DB 2; Length 569;
Best Local Similarity 38.1%; Pred. No. 4.8e-44;
Matches 169; Conservative 76; Mismatches 172; Indels 27; Gaps 12;

Qy 7 GATTLVLVAVGPWLSAAAGGNLSPQKVEVDIIDNFTLRNWRSDSVGNTVFSDYQ 66
Db 9 GRLLAAVLLCVLVVSRCCAGTNLSPQDIQVAVNTNFTLMNNTGDTG-NTVFSAQYQ 67

67 -----KTGMNDWIKLSGCONITSTKCNFSLKLNVEEIKLRIRAE-KENTSSWYEVDSF 120
Db CFDDLQTSPEWKELSGQNVSHTECFSSAITAYYDTHIRIRAEERAKSPWSSIFEM 127

121 TPRKAGIQGPPEVHLEAEDKAIVIHISPGTKDSV--MWALDGLSFTYSLLIWKNSSGVEE 178
Db IPYEIAQIGPPETALQSGAINGAINKINISPPPEANQVRKMW-LISVFFKYNVVDNNSNV-E 185

179 RIENIYSRHKIKLSPETTYCLVKYKAAALLTSWKIGVYSPVHCIKTTVE-NELPPPENIEV 237
Db KVSILPIDVINDLAPETTYCLVKQATVPLEKGLFSPHICIKTRKVDNLLCPTNVRV 245

238 SVONQNTVLKWDYTY-ANMTFQVQWLHAFKRNPGNHLKWKQIOPDCENVKTTQC----- 291
Db FALNMKFYLLWNNHNEHYVTYQYLTGYLKNLYDDYSKWKQVSGCENITSMKCNLSV 305

292 VFPQNVFGKIGYLLRQVQSGNNTSPWSEIKFDETEIQAFLLPPVFNIRSLSDSFHYIG 351
Db IKPTS-----ASYFRVQAMNEYNKSCLSKDVDPPTVNEIGPPDVKVDISDVLHIIKIT 361

361 APQSGNTPTVQDYPPLYEIIFFWNTSNAERKIEKTD---VTVPNLKPLTYVCVKARA 408
Db PPGPGNKMISDLYDFPYQILYWKNSDNEEVEVKMETKQTATVSDLPSTLYCVKQVA 421

409 HTWDEKLNKSSVFSDDAVCEKTKPG 432
Db 422 --FSEAYNKSSDFSRECEIGTAGG 443
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RESULT 15

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Q9PVJ9_CHICK
ID Q9PVJ9_CHICK PRELIMINARY; PRT; 442 AA.
AC Q9PVJ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Interferon alpha/beta receptor 1 (Fragment).
GN Name=IFNAR1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10 receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR EMBL; AF082667; AAD13679.1; -; Genomic DNA.
DR Ensembl; ENSGALG00000015942; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR00282; Cytok receptor_2.
DR InterPro; IPR003961; FN_III.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 4.
DR PROSITE; PS50853; FN3; 4.
KW Receptor.
FT NON TER 442 442
SQ SEQUENCE 442 AA; 49877 MW; 839BEB92170609E0 CRC64;

Query Match 29.8%; Score 689.5; DB 2; Length 442;
Best Local Similarity 37.9%; Pred. No. 9.8e-44;
Matches 166; Conservative 77; Mismatches 168; Indels 27; Gaps 12;

Qy 7 GATTLVLVAVGPWLSAAAGGNLSPQKVEVDIIDNFTLRNWRSDSVGNTVFSDYQ 66
Db 9 GRLLAAVLLCVLVVSRCCAGTNLSPQDIQVAVNTNFTLMNNTGDTG-NTVFSAQYQ 67

67 -----KTGMNDWIKLSGCONITSTKCNFSLKLNVEEIKLRIRAE-KENTSSWYEVDSF 120
Db CFDDLQTSPEWKELSGQNVSHTECFSSAITAYYDTHIRIRAEERAKSPWSSIFEM 127

121 TPRKAGIQGPPEVHLEAEDKAIVIHISPGTKDSV--MWALDGLSFTYSLLIWKNSSGVEE 178
Db IPYEIAQIGPPETALQSGAINGAINKINISPPPEANQVRKMW-LISVFFKYNVVDNNSNV-E 185

179 RIENIYSRHKIKLSPETTYCLVKYKAAALLTSWKIGVYSPVHCIKTTVE-NELPPPENIEV 237
Db KVSILPIDVINDLAPETTYCLVKQATVPLEKGLFSPHICIKTRKVDNLLCPTNVRV 245

238 SVONQNTVLKWDYTY-ANMTFQVQWLHAFKRNPGNHLKWKQIOPDCENVKTTQC----- 291
Db FALNMKFYLLWNNHNEHYVTYQYLTGYLKNLYDDYSKWKQVSGCENITSMKCNLSV 305

292 VFPQNVFGKIGYLLRQVQSGNNTSPWSEIKFDETEIQAFLLPPVFNIRSLSDSFHYIG 351
Db IKPTS-----ASYFRVQAMNEYNKSCLSKDVDPPTVNEIGPPDVKVDISDVLHIIKIT 361

361 APQSGNTPTVQDYPPLYEIIFFWNTSNAERKIEKTD---VTVPNLKPLTYVCVKARA 408
Db PPGPGNKMISDLYDFPYQILYWKNSDNEEVEVKMETKQTATVSDLPSTLYCVKQVA 421

409 HTWDEKLNKSSVFSDDAVC 426
Db 422 --FSEAYNKSSDFSRECE 437

Search completed: January 17, 2006, 07:18:42
Job time : 124.892 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:10:37 ; Search time 30.1828 Seconds  
(without alignments)  
1098.405 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427

Perfect score: 2141

Sequence: 1 GKNLKSPQKVEVDIIDNFI.....AHTMDEKLKNSVFSFPAVCE 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
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  - 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pap:\*
  - 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pap:\*
  - 4: /cgn2\_6/ptodata/1/iaa/PCUS\_COMB.pap:\*
  - 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pap:\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	100.0	434	1	US-08-328-256-11
2	2141	100.0	436	1	US-08-307-588-2
3	2141	100.0	436	2	US-07-971-834-2
4	2141	100.0	436	2	US-09-240-675-2
5	2141	100.0	557	1	US-08-328-256-10
6	2141	100.0	557	1	US-08-471-454-2
7	2141	100.0	557	1	US-08-466-974-2
8	2141	100.0	557	1	US-08-471-453-2
9	2141	100.0	557	1	US-08-307-588-4
10	2141	100.0	557	2	US-07-971-834-4
11	2141	100.0	557	2	US-09-240-675-4
12	2141	100.0	557	2	US-09-949-016-5972
13	2138	99.9	575	2	US-09-949-016-8640
14	2124	99.2	631	2	US-09-056-461-22
15	2089	97.6	496	1	US-08-328-256-12
16	1093	51.1	226	2	US-08-871-572B-10
17	1048	48.9	224	2	US-08-871-572B-9
18	707	33.0	224	2	US-08-871-572B-13
19	672.5	31.4	227	2	US-08-871-572B-14
20	513.5	24.0	224	2	US-08-871-572B-11
21	490.5	22.9	202	4	PCT-US94-14277-3
22	452.5	21.1	219	2	US-08-871-572B-12
23	438.5	20.5	200	4	PCT-US94-14277-4
24	222	10.4	233	2	US-08-871-572B-8
25	220	10.3	273	2	US-09-949-016-11056
26	220	10.3	325	1	US-08-683-743-4
27	220	10.3	325	2	US-09-870-574-3

28	220	10.3	325	2	US-09-265-540E-6	Sequence 6, Appli
29	214	10.0	199	2	US-10-090-365-35	Sequence 35, Appl
30	214	10.0	199	2	US-09-728-911-35	Sequence 35, Appl
31	199	9.3	332	4	PCT-US94-14277-2	Sequence 2, Appli
32	192	9.0	223	4	PCT-US94-14277-6	Sequence 6, Appli
33	182	8.5	567	2	US-09-949-016-11502	Sequence 11502, A
34	180	8.4	553	1	US-08-943-087-2	Sequence 2, Appli
35	180	8.4	553	1	US-08-943-087-14	Sequence 14, Appl
36	180	8.4	553	1	US-08-943-087-16	Sequence 16, Appl
37	180	8.4	553	1	US-08-943-087-18	Sequence 18, Appl
38	180	8.4	553	1	US-08-943-087-20	Sequence 20, Appl
39	180	8.4	553	1	US-08-943-087-22	Sequence 22, Appl
40	180	8.4	553	1	US-08-943-087-24	Sequence 24, Appl
41	180	8.4	553	1	US-08-943-087-26	Sequence 26, Appl
42	180	8.4	553	1	US-08-943-087-28	Sequence 28, Appl
43	180	8.4	553	1	US-08-943-087-30	Sequence 30, Appl
44	180	8.4	553	1	US-08-943-087-32	Sequence 32, Appl
45	180	8.4	553	1	US-08-943-087-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1  
US-08-328-256-11  
; Sequence 11, Application US/08328256  
; Patent No. 5643749  
; GENERAL INFORMATION:  
; APPLICANT: REVEL, Michel  
; APPLICANT: ABRAMOVICH, Carolina  
; APPLICANT: RATOVITSKI, Edward  
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,256  
; FILING DATE: 24-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107378  
; FILING DATE: 24-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: REVEL=13  
; REFERENCE/DOCKET NUMBER: 25,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 434 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-328-256-11

Query Match 100.0%; Score 2141; DB 1; Length 434;  
Best Local Similarity 100.0%; Pred. No. 4.8e-213;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDI IDNFI LRWRNRSDES VGNVTFSDYQKTGMDNWKLSGCONITSTK 60  
Db 27 GKNLKSPQKVEVDI IDNFI LRWRNRSDES VGNVTFSDYQKTGMDNWKLSGCONITSTK 86  
Qy 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQI GPPVHLEAEDKAI VIHI 120  
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQI GPPVHLEAEDKAI VIHI 146  
Qy 121 SPGTKDSVMALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGTKDSVMALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 266  
Qy 241 KRNPGNHLYKWQI PDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSFWSSEEIKFDT 300  
Db 267 KRNPGNHLYKWQI PDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSFWSSEEIKFDT 326  
Qy 301 EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFS DAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFS DAVCE 427

## RESULT 2

US-08-307-588-2  
; Sequence 2, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 436 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-307-588-2

Query Match 100.0%; Score 2141; DB 1; Length 436;  
Best Local Similarity 100.0%; Pred. No. 4.8e-213;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSPQKVEVDI IDNFI LRWRNRSDES VGNVTFSDYQKTGMDNWKLSGCONITSTK 60  
Db 27 GKNLKSPQKVEVDI IDNFI LRWRNRSDES VGNVTFSDYQKTGMDNWKLSGCONITSTK 86  
Qy 61 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQI GPPVHLEAEDKAI VIHI 120  
Db 87 CNFSSKLNVYEEIKLRIRAEKENTSSWYEVDSFTPRKQI GPPVHLEAEDKAI VIHI 146  
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Db 147 SPGTKDSVMALDGLSFTYSLLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVYLVKWDYTYANMTFQVWLHAF 266  
Qy 241 KRNPGNHLYKWQI PDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSFWSSEEIKFDT 300  
Db 267 KRNPGNHLYKWQI PDCENVKTTQCVFPQNVFQKGIYLLRVOASDGNNTSFWSSEEIKFDT 326  
Qy 301 EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIQAFLLPPVFNIRSLSDSFHIIYGAPKQSGNTFVIQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFS DAVCE 401  
Db 387 KKTDTVPNLKPLTVYCVKARAHTMDEKLNKSSVFS DAVCE 427

## RESULT 3

US-07-971-834-2  
; Sequence 2, Application US/07971834  
; Patent No. 6475983  
; GENERAL INFORMATION:  
; APPLICANT: EID, Pierre  
; APPLICANT: GRESSER, Ion  
; APPLICANT: LUTFALLA, Georges  
; APPLICANT: MEYER, Francois  
; APPLICANT: MOGENSEN, Knud E.  
; APPLICANT: TOVEY, Michael  
; APPLICANT: UZE, Gilles  
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH  
; TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/971,834  
; FILING DATE: 17-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR91/00318  
; FILING DATE: 17-APR-1991  
; ATTORNEY/AGENT INFORMATION:



```

; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EID=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-971-834-2

Query Match 100.0%; Score 2141; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 4.8e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKILKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCNQITSTK 60
Db 27 GKILKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCNQITSTK 86
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Db 87 CNFSSLLKNVYEETKLRIRAEKENTSSWYEVDSFTPRKQIGPPEVHLEAEDKAIYIHI 146
Qy 121 SPGTGDSVMALDGLSFTSYLLIWNKSSGVEERIENIYSRHKIYKLSPEITCYCLKVKAAL 180
Db 147 SPGTGDSVMALDGLSFTSYLLIWNKSSGVEERIENIYSRHKIYKLSPEITCYCLKVKAAL 206
Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSSEIKPDT 300
Db 267 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSSEIKPDT 326
Qy 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPLIYIIFWENTSNARKEIIE 360
Db 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPLIYIIFWENTSNARKEIIE 386
Qy 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 4
US-09-240-675-2
; Sequence 2, Application US/09240675
; Patent No. 6787634
; GENERAL INFORMATION:
; APPLICANT: BENOIT, Patrick
; APPLICANT: MEYER, Francois
; APPLICANT: MAGUIRE, Deborah
; APPLICANT: PLAVEC, Ivan
; APPLICANT: TOVEY, Michael G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
; TITLE OF INVENTION: INTERFERON
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,675
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,588
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: PCT/EP93/00770
; FILING DATE: 30-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92400902.0
; FILING DATE: 31-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 436 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-240-675-2

Query Match 100.0%; Score 2141; DB 2; Length 436;
Best Local Similarity 100.0%; Pred. No. 4.8e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKILKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCNQITSTK 60
Db 27 GKILKSPQKVEVDIIDNFILRWNRSDSVGNVTFSDYQKTGMDNWKLSGCCNQITSTK 86
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Db 87 CNFSSLLKNVYEETKLRIRAEKENTSSWYEVDSFTPRKQIGPPEVHLEAEDKAIYIHI 146
Qy 121 SPGTGDSVMALDGLSFTSYLLIWNKSSGVEERIENIYSRHKIYKLSPEITCYCLKVKAAL 180
Db 147 SPGTGDSVMALDGLSFTSYLLIWNKSSGVEERIENIYSRHKIYKLSPEITCYCLKVKAAL 206
Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 240
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNYVVKWDYTYANMTFQVQWLHAF 266
Qy 241 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSSEIKPDT 300
Db 267 KRNPNGHLYKWKQIPDCENVKTTQCVFPQNVFQGIYLLRVQASDGNNTSFWSSEIKPDT 326
Qy 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPLIYIIFWENTSNARKEIIE 360
Db 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPLIYIIFWENTSNARKEIIE 386
Qy 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401
Db 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 5
US-08-328-256-10
; Sequence 10, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300

```

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; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL=13
; REFERENCE/DOCKET NUMBER: 25,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-328-256-10

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Query Match      100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7,1e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKMLKSPQKVEVDIIDNFILRNRSDESQVNTFSDYQKTGMNDWIKLSGCONITSTK 60
Db 27 GKMLKSPQKVEVDIIDNFILRNRSDESQVNTFSDYQKTGMNDWIKLSGCONITSTK 86
Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 120
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 146
Qy 121 SPGTQDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
Db 147 SPGTQDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAPL 240
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAPL 266
Qy 241 KRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300
Db 267 KRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326
Qy 301 EIOAFLLPVPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKIIIE 360
Db 327 EIOAFLLPVPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKIIIE 386
Qy 361 KKTDTVTPNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401
Db 387 KKTDTVTPNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 427

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## RESULT 6

```

US-08-471-454-2
; Sequence 2, Application US/08471454
; Patent No. 5731169
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges

```

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; APPLICANT: GRESSER, Ion
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,454
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BYENE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-471-454-2

Query Match      100.0%; Score 2141; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 7,1e-213;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKMLKSPQKVEVDIIDNFILRNRSDESQVNTFSDYQKTGMNDWIKLSGCONITSTK 60
Db 27 GKMLKSPQKVEVDIIDNFILRNRSDESQVNTFSDYQKTGMNDWIKLSGCONITSTK 86
Qy 61 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 120
Db 87 CNFSSSLKLVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 146
Qy 121 SPGTQDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
Db 147 SPGTQDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
Qy 181 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAPL 240
Db 207 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAPL 266
Qy 241 KRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 300
Db 267 KRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKPDT 326
Qy 301 EIOAFLLPVPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKIIIE 360
Db 327 EIOAFLLPVPVFNIRSLSDSFHIYIGAPKQSGNTPIQDYPLIYELIIFWNTSNAERKIIIE 386
Qy 361 KKTDTVTPNKLPLTVYCVKARAHTMDEKLNKSSVFSFSDAVCE 401

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Db 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 7

US-08-466-974-2

; Sequence 2, Application US/08466974

; Patent No. 5861258

; GENERAL INFORMATION:

; APPLICANT: MOGENSEN, Knud E.

; APPLICANT: UZE, Gilles

; APPLICANT: LUTFALLA, Georges

; APPLICANT: GRESSER, Ion

; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,974

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/900,642

; FILING DATE: 15-JUN-1992

; APPLICATION NUMBER: FR 89/13770

; FILING DATE: 20-OCT-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: BYRNE, THOMAS E.

; REGISTRATION NUMBER: 32,205

; REFERENCE/DOCKET NUMBER: 960-7

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-466-974-2

Query Match 100.0%; Score 2141; DB 1; Length 557;

Best Local Similarity 100.0%; Pred. No. 7.1e-213;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILNRNRSDESGVNTFSEFDYQKTGMNDWIKLSGCONITSTK 60

Db 27 GKNLSPQKVEVDIIDDNFILNRNRSDESGVNTFSEFDYQKTGMNDWIKLSGCONITSTK 86

Qy 61 CNFSLKLVNVEIKLRIRAEKNTSSWYEVDSFTFPRKQAIQGPVEHLEADKAIIVHI 120

Db 87 CNFSLKLVNVEIKLRIRAEKNTSSWYEVDSFTFPRKQAIQGPVEHLEADKAIIVHI 146

Qy 121 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVBERIENIYSRHKIYKLSPTTYCLKVKAAL 180

Db 147 SPGTKDSVMWALDGLSFTYSLLIWNKSSGVBERIENIYSRHKIYKLSPTTYCLKVKAAL 206

Qy 181 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANMTFQVOWLHAF 240

Db 207 LTSWKIGYSPVHCIKTTVENELPPENIEVSQNVQNTVVKWDYTYANMTFQVOWLHAF 266

Qy 241 KRNPGNHLYKWKQIPDCENVKTTQCVPFQPNVQKGIYLLRVQASDGNNTSFWSSEIKPDT 300

Db 267 KRNPGNHLYKWKQIPDCENVKTTQCVPFQPNVQKGIYLLRVQASDGNNTSFWSSEIKPDT 326

Qy 301 EIOAFLLPVPFNIRSLSDSFHYIGAPKQSGNTPVIQDYPLIYELIIFWENTSNAERKIIIE 360

Db 327 EIOAFLLPVPFNIRSLSDSFHYIGAPKQSGNTPVIQDYPLIYELIIFWENTSNAERKIIIE 386

Qy 361 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401

Db 387 KKTDTVTPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 427

RESULT 8

US-08-471-453-2

; Sequence 2, Application US/08471453

; Patent No. 5886153

; GENERAL INFORMATION:

; APPLICANT: MOGENSEN, Knud E.

; APPLICANT: UZE, Gilles

; APPLICANT: LUTFALLA, Georges

; APPLICANT: GRESSER, Ion

; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,453

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/900,642

; FILING DATE: 15-JUN-1992

; APPLICATION NUMBER: FR 89/13770

; FILING DATE: 20-OCT-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: BYRNE, THOMAS E.

; REGISTRATION NUMBER: 32,205

; REFERENCE/DOCKET NUMBER: 960-7

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-471-453-2

Query Match 100.0%; Score 2141; DB 1; Length 557;

Best Local Similarity 100.0%; Pred. No. 7.1e-213;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILNRNRSDESGVNTFSEFDYQKTGMNDWIKLSGCONITSTK 60

Db 27 GKNLSPQKVEVDIIDDNFILNRNRSDESGVNTFSEFDYQKTGMNDWIKLSGCONITSTK 86

Qy 61 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 120  
Db 87 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 146  
Qy 121 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 180  
Db 147 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 206  
Qy 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQWLHAF 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
Qy 301 EIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSVDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSVDAVCE 427

## RESULT 9

US-08-307-588-4  
; Sequence 4, Application US/08307588  
; Patent No. 5919453  
; GENERAL INFORMATION:  
; APPLICANT: BENOIT, Patrick  
; APPLICANT: MEYER, Francois  
; APPLICANT: MAGUIRE, Deborah  
; APPLICANT: PLAVEC, Ivan  
; APPLICANT: TOVEY, Michael G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
; TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I  
; TITLE OF INVENTION: INTERFERON  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/307,588  
; FILING DATE: 05-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/00770  
; FILING DATE: 30-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 92400902.0  
; FILING DATE: 31-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-307-588-4

Query Match 100.0%; Score 2141; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 7.1e-213; Indels 0; Gaps 0;  
Matches 401; Conservative 0; Mismatches 0;  
Qy 1 GKNLKSPQKQVEVDIIDNFIILRWNRSDSVGNVTFSPDYQKTGMNDWIKLSGCONITSTK 60  
Db 27 GKNLKSPQKQVEVDIIDNFIILRWNRSDSVGNVTFSPDYQKTGMNDWIKLSGCONITSTK 86  
Qy 61 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 120  
Db 87 CNFSSKLVNVEIKLIRAEKENTSSWYEVDSFTPRKQAIQGPPEVHLEAEDKAIIVHI 146  
Qy 121 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 180  
Db 147 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEITTYCLKVAAL 206  
Qy 181 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGVSPVHCITKTVENELPPENIEVSQNVQNYLVKWDYTYANMTFQVQWLHAF 266  
Qy 241 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
Qy 301 EIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKII 360  
Db 327 EIOAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSVDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSVDAVCE 427

## RESULT 10

US-07-971-834-4  
; Sequence 4, Application US/07971834  
; Patent No. 6475983  
; GENERAL INFORMATION:  
; APPLICANT: EID, Pierre  
; APPLICANT: GRESSER, Ion  
; APPLICANT: LUTFALLA, Georges  
; APPLICANT: MEYER, Francois  
; APPLICANT: MOGENSEN, Knud E.  
; APPLICANT: TOVEY, Michael  
; APPLICANT: UZE, Gilles  
; TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH  
; TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/971,834  
; FILING DATE: 17-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR91/00318  
; FILING DATE: 17-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: EID=1  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-971-834-4

Query Match 100.0%; Score 2141; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 7.1e-213;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNDWIKLSCQNIITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNDWIKLSCQNIITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 146  
Qy 121 SPGKDSVMWALDGLSFTYSLLIWNSSGVVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGKDSVMWALDGLSFTYSLLIWNSSGVVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 206  
Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVQWLHAF 266  
Qy 241 KRNPENHLYKWKQIPDCENVKTCQVFPQNVFQKGIYLLRVQASDGNNTSFWSEIKEDT 300  
Db 267 KRNPENHLYKWKQIPDCENVKTCQVFPQNVFQKGIYLLRVQASDGNNTSFWSEIKEDT 326  
Qy 301 BIAQFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKILIE 360  
Db 327 BIAQFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKILIE 386  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSADVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSADVCE 427

RESULT 11

US-09-240-675-4  
Sequence 4, Application US/09240675  
Patent No. 6787634

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick  
APPLICANT: MEYER, Francois  
APPLICANT: MAGUIRE, Deborah  
APPLICANT: PLAVEC, Ivan  
APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

TITLE OF INVENTION: INTERFERON

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,675

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588  
FILING DATE: 05-DEC-1994  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-240-675-4

Query Match 100.0%; Score 2141; DB 2; Length 557;

Best Local Similarity 100.0%; Pred. No. 7.1e-213;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNDWIKLSCQNIITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRNRSDESNGVNTFSFDYQKTGMNDWIKLSCQNIITSTK 86  
Qy 61 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 120  
Db 87 CNFSSLKLVNVEEIKLIRAEKENTSSWYEVDSFTPFKAQIGPPEVHLEAEDKAIVIH 146  
Qy 121 SPGKDSVMWALDGLSFTYSLLIWNSSGVVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 180  
Db 147 SPGKDSVMWALDGLSFTYSLLIWNSSGVVEERIENIYSRHKIYKLSPTTYCLVKVKAAL 206  
Qy 181 LTSWKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSVQNVYLVKWDYTYANMTFQVQWLHAF 266  
Qy 241 KRNPENHLYKWKQIPDCENVKTCQVFPQNVFQKGIYLLRVQASDGNNTSFWSEIKEDT 300  
Db 267 KRNPENHLYKWKQIPDCENVKTCQVFPQNVFQKGIYLLRVQASDGNNTSFWSEIKEDT 326  
Qy 301 BIAQFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKILIE 360  
Db 327 BIAQFLPPVFNIRSLSDSFHIYIGAPKQSGNTVPVQDYPLIYELIIFWENTSNAERKILIE 386  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSADVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSADVCE 427

RESULT 12

US-09-949-016-5972

Sequence 5972, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5972  
; LENGTH: 557  
; TYPE: PR1  
; ORGANISM: Human  
US-09-949-016-5972

Query Match 100.0%; Score 2141; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 7.1e-213;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDNFIILNRSDSVGNVTFSDYQKTMNDWIKLGGCQNTSTK 60  
Db 27 GKNLKSQKVEVDIIDNFIILNRSDSVGNVTFSDYQKTMNDWIKLGGCQNTSTK 86  
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPEVHLEAEDKAIYIHI 120  
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPEVHLEAEDKAIYIHI 146  
Qy 121 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNYVVKWDTYANMTFQVWLHAF 240  
Db 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNYVVKWDTYANMTFQVWLHAF 266  
Qy 241 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 267 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 326  
Qy 301 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPYIYELIIFWENTSNAERKII 360  
Db 327 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPYIYELIIFWENTSNAERKII 386  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427

RESULT 13  
US-09-949-016-8640  
; Sequence 8640, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8640  
; LENGTH: 575  
; TYPE: PR1  
; ORGANISM: Human  
US-09-949-016-8640

Query Match 99.9%; Score 2138; DB 2; Length 575;  
Best Local Similarity 99.8%; Pred. No. 1.5e-212;  
Matches 400; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKNLKSQKVEVDIIDNFIILNRSDSVGNVTFSDYQKTMNDWIKLGGCQNTSTK 60  
Db 45 GKNLKSQKVEVDIIDNFIILNRSDSVGNVTFSDYQKTMNDWIKLGGCQNTSTK 104

Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPEVHLEAEDKAIYIHI 120  
Db 105 CNFSSKLNVYEEIKLIRAEKENTSSWYEVDSFTPRKQAIIGPEVHLEAEDKAIYIHI 164  
Qy 121 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 165 SPGKDSVMALDGLSFTYSLIWKNSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 224  
Qy 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNYVVKWDTYANMTFQVWLHAF 240  
Db 225 LTSWKIGVSPVHCIKTTVENELPPENIEVSVQNYVVKWDTYANMTFQVWLHAF 284  
Qy 241 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 300  
Db 285 KRNPENHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSSEIKFDT 344  
Qy 301 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPYIYELIIFWENTSNAERKII 360  
Db 345 EIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTFVIQDYPYIYELIIFWENTSNAERKII 404  
Qy 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
Db 405 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 445

RESULT 14  
US-09-056-461-22  
; Sequence 22, Application US/09056461  
; Patent No. 6713609  
; GENERAL INFORMATION:  
; APPLICANT: Chunharapai, Anon  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Love, Richard B.  
; APPLICANT: Lu, Ji  
; APPLICANT: Stewart, Timothy A.  
; TITLE OF INVENTION: Type I Interferon Receptor Antibodies  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,461  
; FILING DATE: 07-Apr-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/058212  
; FILING DATE: 16  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1039P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 631 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-056-461-22

Query Match 99.2%; Score 2124; DB 2; Length 631;  
Best Local Similarity 100.0%; Pred. No. 5e-211;  
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSGCONITSTKCNF 63  
DB 1 LKSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSGCONITSTKCNF 60  
QY 64 SSLKLVYVEEIKLIRAEKENTSSWYEVDSFTPRKQAGIGPEVHLEAEDKAIIVHISPG 123  
DB 61 SSLKLVYVEEIKLIRAEKENTSSWYEVDSFTPRKQAGIGPEVHLEAEDKAIIVHISPG 120  
QY 124 TKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEPTYCYLKVKAAALTS 183  
DB 121 TKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEPTYCYLKVKAAALTS 180  
QY 184 WKIGYSPVHCICKTTVENELPPENIEVSQVQNYVLKWDYTYANMTFQVQWLHAFKRN 243  
DB 181 WKIGYSPVHCICKTTVENELPPENIEVSQVQNYVLKWDYTYANMTFQVQWLHAFKRN 240  
QY 244 PGNHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKFDTEIQ 303  
DB 241 PGNHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKFDTEIQ 300  
QY 304 AFLPPVFNIRSLSDSFHIIYIGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERKIIIEKT 363  
DB 301 AFLPPVFNIRSLSDSFHIIYIGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERKIIIEKT 360  
QY 364 DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 361 DVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 398

## RESULT 15

US-08-328-256-12  
; Sequence 12, Application US/08328256  
; Patent No. 5643749  
; GENERAL INFORMATION:  
; APPLICANT: REVEL, Michel  
; APPLICANT: ABRAMOVICH, Carolina  
; APPLICANT: RATOVITSKI, Edward  
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,256  
; FILING DATE: 24-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107378  
; FILING DATE: 24-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: REVEL=13  
; REFERENCE/DOCKET NUMBER: 25,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 496 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-328-256-12

Query Match 97.6%; Score 2089; DB 1; Length 496;  
Best Local Similarity 98.0%; Pred. No. 1.5e-207;  
Matches 393; Conservative 0; Mismatches 0; Indels 8; Gaps 1;  
QY 1 GKNLKSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSGCONITSTK 60  
DB 27 GKNLKSPQKVEVDIIDDNFILRNWRSDES VGNVTFSDYQKTGMNDWIKLSGCONITSTK 86  
QY 61 CNFSSKLVNVEEIKLIRAEKENTSSWYEVDSFTPRKQAGIGPEVHLEAEDKAIIVHIS 120  
DB 87 CNFSSKLVNVEEIKLIRAEKENTSSWYEVDSFTPRKQAGIGPEVHLEAEDKAIIVHIS 146  
QY 121 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEPTYCYLKVKAAAL 180  
DB 147 SPGTKDSVMALDGLSTYSLLIWNSSGVEERIENIYSRHKIYKLSPEPTYCYLKVKAAAL 206  
QY 181 LTSWKIGYSPVHCICKTTVENELPPENIEVSQVQNYVLKWDYTYANMTFQVQWLHAFK 240  
DB 207 LTSWKIGYSPVHCICKTTVENELPPENIEVSQVQNYVLKWDYTYANMTFQVQWLHAFK 266  
QY 241 KRNPNGHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKFD 300  
DB 267 KRNPNGHLYKWKQIIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFSWSEIKFD 326  
QY 301 EIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERK 360  
DB 327 EIQAFLLPPVFNIRSLSDSFHIIYIGAPKQSGNTPTVIQDYPLIYBIIIFWENTSNAERK 386  
QY 361 KKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401  
DB 387 KKTDTVTPNLKPLTVYCVKARAHTMDE-----SDAVCE 419

Search completed: January 17, 2006, 07:20:57  
Job time : 31.1828 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 06:24:56 ; Search time 135 Seconds  
(without alignments)  
1419.031 Million cell updates/sec

Title: US-10-824-981-2  
Perfect score: 2313  
Sequence: 1 MMVLGGATTLVAVGPV.....KSSVFSDAVCEKFGNTSK 436

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2313	100.0	436	2 AAR14487	Aar14487 Soluble i
2	2313	100.0	436	2 AAR28495	Aar28495 Sequence
3	2313	100.0	436	6 ABU05090	Abu05090 Human exp
4	2313	100.0	436	6 ABU05092	Abu05092 Human exp
5	2313	100.0	436	6 ABU05098	Abu05098 Human exp
6	2313	100.0	557	2 AAR14488	Aar14488 Complete
7	2313	100.0	557	2 AAR11958	Aar11958 Human alp
8	2313	100.0	557	2 AAR28496	Aar28496 Sequence
9	2313	100.0	557	2 AAR42635	Aar42635 Human int
10	2313	100.0	557	6 ABU05091	Abu05091 Human exp
11	2313	100.0	557	6 ABU05094	Abu05094 Human exp
12	2313	100.0	557	6 ABU05107	Abu05107 Human exp
13	2313	100.0	557	6 ABU05099	Abu05099 Human exp
14	2313	100.0	557	6 ABU05106	Abu05106 Human exp
15	2313	100.0	557	6 ABU05097	Abu05097 Human exp
16	2313	100.0	557	6 ABU05093	Abu05093 Human exp
17	2313	100.0	557	6 ABU05100	Abu05100 Human exp
18	2313	100.0	575	8 ADR666319	Adr666319 Human pro
19	2313	100.0	575	8 ADR66661	Adr66661 Human pro
20	2309	99.8	557	6 AAR75356	Aar75356 Human IFN
21	2309	99.8	557	6 ABU05102	Abu05102 Human exp
22	2308	99.8	557	2 AAW21804	Aaw21804 Transmemb
23	2308	99.8	557	6 ABU05103	Abu05103 Human exp
24	2307	99.7	557	6 ABU05095	Abu05095 Human exp

25	2304	99.6	436	2 AAR71723	Aar71723 IFN recep
26	2304	98.6	436	6 ABU05101	Abu05101 Human exp
27	2302	99.5	575	3 AAB57094	Aab57094 Human pro
28	2302	99.5	575	6 ABU05096	Abu05096 Human exp
29	2287	98.9	575	4 ABG17294	Abg17294 Novel hum
30	2279	98.5	441	9 ADV25067	Adv25067 INR1_T11
31	2260	97.7	434	2 AAW21805	Aaw21805 Spliced-d
32	2260	97.7	434	6 ABU05104	Abu05104 Human exp
33	2208	95.5	496	2 AAW21806	Aaw21806 Spliced-d
34	2208	95.5	496	6 ABU05105	Abu05105 Human exp
35	2158	93.3	631	8 ADK23579	Adk23579 Human IFN
36	1725.5	74.6	458	8 ADH22370	Adh22370 Human rec
37	916	39.6	187	8 ADH22369	Adh22369 Human rec
38	236.5	10.2	273	6 ABR38950	AbR38950 Human AK1
39	234.5	10.1	273	6 ABR38949	AbR38949 Human AK1
40	233.5	10.1	220	5 AAU76911	Aau76911 Human cyt
41	233.5	10.1	220	8 ADS31753	Ads31753 Human CRF
42	233.5	10.1	220	8 ADS92755	Ads92755 Human CRF
43	233.5	10.1	273	6 ABR38944	AbR38944 Human AK1
44	233.5	10.1	476	5 AAR76912	Aar76912 Human CRF
45	233.5	10.1	476	6 AAE30845	Aae30845 Human CRF

## ALIGNMENTS

RESULT 1  
AAR14487  
ID AAR14487 standard; protein; 436 AA.  
XX AC AAR14487;  
XX DT 16-JAN-1992 (first entry)  
XX DE Soluble interferon-alpha/beta receptor.  
XX KW IFN; autoimmune disease; graft rejection; histocompatibility.  
XX OS Homo sapiens.  
XX PN FR2657881-A.  
XX PD 09-AUG-1991.  
XX PF 05-FEB-1990; 90FR-00001298.  
XX PR 05-FEB-1990; 90FR-00001298.  
XX PA (EUBI-) LAB EURO BIOTECHNO.  
XX Bid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey MG;  
XX Uze G;  
XX WPI; 1991-319778/44.  
XX N-PSDB; AAQ14239.  
XX PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
XX used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
XX anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
XX PS Claim 2; Page 45; 52pp; French.  
XX CC The transmembrane and cytoplasmic domains of the native IFN receptor have  
XX been deleted to obtain a soluble, circulating form of the receptor.  
XX CC Potentially immunogenic epitopes have thus been eliminated. Derivatives  
XX obtained by substitution or deletion of this sequence are also claimed as  
XX are hybrid molecules comprising the soluble receptor (or deriv.) and an  
XX immunoglobulin such as IgG1. See also AAQ14240  
XX SQ Sequence 436 AA;  
XX Query Match 100.0%; Score 2313; DB 2; Length 436;  
XX Best Local Similarity 100.0%; Pred. No. 7e-200;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNT 60  
DB 1 MMVLLGATTLVLAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120  
QY 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
DB 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
QY 241 NQNYVLKWDYTYANMTFOVQLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
DB 241 NQNYVLKWDYTYANMTFOVQLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
QY 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
DB 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 2  
AAR28495  
ID AAR28495 standard; protein; 436 AA.  
XX  
AC AAR28495;  
XX  
DT 25-MAR-2003 (revised)  
DT 31-MAR-1993 (first entry)  
XX  
DE Sequence of a soluble form of the interferon (IFN) receptor with a high  
DE affinity for IFN-alpha and -beta.  
XX  
KW Interferon receptor; alpha-interferon; beta-interferon.  
XX  
OS Synthetic.  
XX  
PN WO9218626-A1.  
XX  
PD 29-OCT-1992.  
XX  
PF 17-APR-1991; 91WO-FR000318.  
XX  
PR 17-APR-1991; 91WO-FR000318.  
XX  
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.  
XX  
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
PI Uze G;  
XX  
XX WPI; 1992-382110/46.  
DR N-PSDB; AAQ30532.  
XX  
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
PT useful as immunosuppressants, for treating autoimmune diseases and  
PT transplant rejection.  
XX  
PS Claim 2; Fig 1; 58pp; English.  
XX

CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
CC primers and cloned cDNA as template. For example, bacteriophage lambda  
CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
CC receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.  
CC AAR28496 represents the complete receptor. AAR28495 lacks the  
CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
CC diseases and graft rejection. They lack the toxic side-effects of known  
CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ

Sequence 436 AA;

Query Match 100.0%; Score 2313; DB 2; Length 436;  
Best Local Similarity 100.0%; Pred. No. 7e-200;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNT 60  
DB 1 MMVLLGATTLVLAVGPNVLSAAGGNLKSPOKVEVDIIDDNFILRNRSDESVCNT 60  
QY 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120  
DB 61 FSDYQKTGMNDWIKLSCQNTITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEDSF 120  
QY 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
DB 121 TPFRAQIGPPEVHLEARDKAIIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVEERI 180  
QY 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
DB 181 ENIYSRHKIYKLSPEPTYCLKVAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
QY 241 NQNYVLKWDYTYANMTFOVQLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
DB 241 NQNYVLKWDYTYANMTFOVQLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
QY 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
DB 301 GYLLRVQASDGNNTSFWSEEEKFDEIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
DB 361 VIQDYPLIYEIIFWENTSNAERKIEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 421 FSDAVCEKTKPGNTSK 436

RESULT 3

ABU05090  
ID ABU05090 standard; protein; 436 AA.  
XX  
AC ABU05090;  
XX

DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1756.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX

```
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1756; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 436 AA;
SQ
Query Match 100.0%; Score 2313; DB 6; Length 436;
Best Local Similarity 100.0%; Pred. No. 7e-200;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVLLGATTLVLVAVGPVWLSAAGGKLNKSPQKVEVDIIDDNFTLRNRSDESVDNF 60
DB 1 MMVLLGATTLVLVAVGPVWLSAAGGKLNKSPQKVEVDIIDDNFTLRNRSDESVDNF 60
QY 61 PSFDYQKGMWNWIKLGGQNTSTKCNFSSKLNVYRKIRAEKENTSSWYVDQSF 120
DB 61 PSFDYQKGMWNWIKLGGQNTSTKCNFSSKLNVYRKIRAEKENTSSWYVDQSF 120
QY 121 TFRKRAIQGPPEVHLEAEKAIVIHISPTGKDSVMWALDGLSPTYLLWKNSSGVVEIRI 180
DB 121 TFRKRAIQGPPEVHLEAEKAIVIHISPTGKDSVMWALDGLSPTYLLWKNSSGVVEIRI 180
QY 181 ENIYSRHKYKLSPTETCYLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240
DB 181 ENIYSRHKYKLSPTETCYLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240
QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPPQNVQK 300
DB 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPPQNVQK 300
QY 301 GYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPVFNIRSLSDSPHIVIGAPKQSGNTP 360
DB 301 GYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPVFNIRSLSDSPHIVIGAPKQSGNTP 360
QY 361 VIQDYLPIYEIIFWNTSNAERKIEKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
DB 361 VIQDYLPIYEIIFWNTSNAERKIEKKTDTVTVPNLKPLTYVCVKARAHMTDEKLNKSSV 420
```

```
QY 421 FSDAVCEKTKPGNTSK 436
DB 421 FSDAVCEKTKPGNTSK 436
RESULT 4
ABU05092
ID ABU05092 standard; protein; 436 AA.
XX
XX AC ABU05092;
XX
XX DT 29-JAN-2003 (first entry)
XX
XX DE Human expressed protein tag (EPT) #1758.
XX
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO200278524-A2.
XX
XX PD 10-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-US009671.
XX
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1758; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 436 AA;
SQ
Query Match 100.0%; Score 2313; DB 6; Length 436;
Best Local Similarity 100.0%; Pred. No. 7e-200;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MMVLLGATTLLVAVGPWVLSAAGGKNLKSPQKVEVDIIDDNFILRNWRSDESGVNT 60  
 Db 1 MMVLLGATTLLVAVGPWVLSAAGGKNLKSPQKVEVDIIDDNFILRNWRSDESGVNT 60  
 QY 61 FSPDYQKTGMDNWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120  
 Db 61 FSPDYQKTGMDNWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120  
 QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
 Db 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPETTYCLVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
 Db 181 ENIYSRHKIYKLSPETTYCLVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 QY 301 GYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
 Db 301 GYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
 QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPITYVCVARAHTMDEKLNKSSV 420  
 Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPITYVCVARAHTMDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 5

ABU05098  
 ID ABU05098 standard; protein; 436 AA.  
 AC ABU05098;  
 XX  
 XX 29-JAN-2003 (first entry)  
 XX Human expressed protein tag (EPT) #1764.  
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW processase; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX Homo sapiens.  
 XX WO200278524-A2.  
 XX 10-OCT-2002.  
 XX 28-MAR-2002; 2002WO-US009671.  
 XX 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-035985P.  
 XX (ZYCO-) ZYCOS INC.  
 XX Chicx RM, Tomlinson AJ, Urban RG;  
 XX WPI; 2003-040607/03.  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.

XX Example 2; SEQ ID NO 1764; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 436 AA;

Query Match 100.0%; Score 2313; DB 6; Length 436;  
 Best Local Similarity 100.0%; Pred. No. 7e-200;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLLVAVGPWVLSAAGGKNLKSPQKVEVDIIDDNFILRNWRSDESGVNT 60  
 Db 1 MMVLLGATTLLVAVGPWVLSAAGGKNLKSPQKVEVDIIDDNFILRNWRSDESGVNT 60

QY 61 FSPDYQKTGMDNWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120

Db 61 FSPDYQKTGMDNWIKLSGQCNITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWYEVDSF 120

QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180

Db 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180

QY 181 ENIYSRHKIYKLSPETTYCLVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240

Db 181 ENIYSRHKIYKLSPETTYCLVKAALLTSWKIGVSPVHCITTVENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300

Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300

QY 301 GYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

Db 301 GYLLRVOASDGNNTSFWSEEEKFDEIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360

QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPITYVCVARAHTMDEKLNKSSV 420

Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPITYVCVARAHTMDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436

Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 6

AAAR14488  
 ID AAAR14488 standard; protein; 557 AA.  
 XX  
 XX AAAR14488;  
 XX  
 XX 16-JAN-1992 (first entry)  
 XX Complete interferon-alpha/beta receptor.  
 DE  
 XX IFN; autoimmune disease; graft rejection; histocompatibility.

XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Domain 437..457  
 FT FT /label= transmembrane  
 FT FT 458..557  
 FT FT /label= cytoplasmic  
 XX FR2657881-A.  
 XX PD 09-AUG-1991.  
 XX PF 05-FEB-1990; 90FR-00001298.  
 XX PR 05-FEB-1990; 90FR-00001298.  
 XX PA (EUBI-) LAB EURO BIOTECHNO.  
 XX PI Bid P, Gresser I, Lutfalla G, Meyer P, Mogensen KE, Tovey MG;  
 XX PI Uze G;  
 XX WPI; 1991-319778/44.  
 XX DR N-PSDB; AAQ14240.  
 XX PT New water-soluble polypeptide(s) with affinity for IFN-alpha and beta -  
 PT used to treat e.g. lupus erythematosus, Behcet's disease, aaaaaplastic  
 PT anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
 XX Disclosure; Page 47; 52pp; French.  
 XX The invention covers derivatives of the interferon-alpha and/or beta  
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains  
 CC of the native receptor or by substitution. Potentially immunogenic  
 CC epitopes are eliminated and the deriv. can be secreted from transformed  
 CC cells. Soluble deriv.s block the activity of IFN alpha/beta and can be  
 CC used to treat autoimmune diseases or to inhibit graft rejection. See also  
 CC AAQ14239  
 XX Sequence 557 AA;  
 SQ Query Match 100.0%; Score 2313; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILRNRSDESIGNVT 60  
 DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILRNRSDESIGNVT 60  
 QY 61 PSFDYQKTGMNDWIKLGGCONITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 DB 61 PSFDYQKTGMNDWIKLGGCONITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENKTKTQCVFPQNVFOK 300  
 DB 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENKTKTQCVFPQNVFOK 300  
 QY 301 GYLRLVQASDGNNTSFWSSEIKFDEIQAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 DB 301 GYLRLVQASDGNNTSFWSSEIKFDEIQAFLPPVFNIRSLSDSPHIYIGAPKQSGNTP 360  
 QY 361 VIQDYPLIYEIIFWNTSNAERKIEBKTDVTPVNLKPLTYCVKARAHTMDEKLNKSSV 420  
 DB 361 VIQDYPLIYEIIFWNTSNAERKIEBKTDVTPVNLKPLTYCVKARAHTMDEKLNKSSV 420

QY 421 FSDAVCEKTKPNTSK 436  
 DB 421 FSDAVCEKTKPNTSK 436  
 RESULT 7  
 AAAR11958  
 ID AAR11958 standard; protein; 557 AA.  
 XX AC AAR11958;  
 XX DT 18-JUL-1991 (first entry)  
 XX DE Human alpha-interferon receptor protein.  
 XX KW Human alpha IFN; IFN agonists; antiviral; anti tumour agent;  
 XX KW drug targeting.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..27  
 FT FT /label= signal peptide  
 XX WO9105862-A.  
 XX PD 02-MAY-1991.  
 XX PF 20-OCT-1989; 89FR-00013770.  
 XX PR 20-OCT-1989; 89FR-00013770.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX PI Mogensen K, Lutfalla G, Gresser I;  
 XX WPI; 1991-148740/20.  
 XX DR N-PSDB; AAQ11701.  
 XX New human alpha-interferon receptor protein - useful for testing  
 FT interferon agonists and in treatment or diagnosis.  
 XX Disclosure; Fig 4; 30pp; French.  
 CC This recombinant human alpha interferon (IFN) receptor protein is useful  
 CC for the testing of IFN agonists and for treatment and diag- nosis of  
 CC viral diseases and tumours. Antibodies raised against this protein can be  
 CC used for blocking the receptor when required, eg where overexpression of  
 CC alpha-IFN is harmful. The Abs are also useful for eg drug targeting.  
 CC Variants of the protein, having residue 164 (Thr) replaced by Arg and an  
 CC Asp inserted between residues 479 and 480, are also useful  
 XX Sequence 557 AA;  
 SQ Query Match 100.0%; Score 2313; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILRNRSDESIGNVT 60  
 DB 1 MMVLLGATTLVLVAVGPWVLSAAAGGNLKSPOKVEVDIIDDNFIILRNRSDESIGNVT 60  
 QY 61 PSFDYQKTGMNDWIKLGGCONITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 DB 61 PSFDYQKTGMNDWIKLGGCONITSTKCNFSSLLKLVYEEIKLIRAEKENTSSWEVDSE 120  
 QY 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240

QY 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 Db |||||  
 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 QY 301 GYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 Db |||||  
 301 GYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 QY 361 VTQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTVYCVKARAHMTDEKLNKSSV 420  
 Db |||||  
 361 VTQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTVYCVKARAHMTDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db |||||  
 421 FSDAVCEKTKPGNTSK 436

## RESULT 8

AAR28496  
 ID AAR28496 standard; protein; 557 AA.

XX AAR28496;  
 AC

XX 25-MAR-2003 (revised)  
 DT 31-MAR-1993 (first entry)

XX Sequence of a soluble form of the interferon (IFN) receptor with a high  
 DE affinity for IFN-alpha and -beta.  
 DE

XX Interferon receptor; alpha-interferon; beta-interferon.  
 KW

XX Synthetic.  
 OS

XX WO9218626-A1.  
 PN

XX 29-OCT-1992.  
 PD

XX 17-APR-1991; 91WO-FR000318.  
 PF

XX 17-APR-1991; 91WO-FR000318.  
 PR

XX (EUBI-) LAB EURO BIOTECHNOLOGIE.  
 PA

XX Bid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE, Tovey M;  
 PI Uze G;  
 PI

XX WPI; 1992-382110/46.  
 DR

XX N-PSDB; AAQ30533.  
 DR

XX Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta -  
 PT useful as immunosuppressants, for treating auto-immune diseases and  
 PT transplant rejection.  
 PT

XX Claim 3; Fig 2; 58pp; English.  
 PS

XX DNA encoding the water-soluble polypeptide with a high affinity for IFN-  
 CC alpha and -beta is isolated by PCR, using appropriate oligonucleotides as  
 CC primers and cloned cDNA as template. For example, bacteriophage lambda  
 CC ZAP, containing the entire coding sequence of the IFN-alpha and -beta  
 CC receptor (AAQ30533), was incubated with oligos AAQ30534 and AAQ30535.  
 CC AAR28496 represents the complete receptor. AAR28495 lacks the  
 CC transmembrane and cytoplasmic domains. Both forms bind IFN in the same  
 CC way as antibodies so are immunosuppressants e.g. for treating autoimmune  
 CC diseases and graft rejection. They lack the toxic side-effects of known  
 CC immunosuppressants such as steroids. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 CC

XX Sequence 557 AA;  
 SQ

Query Match

Best Local Similarity 100.0%; Score 2313; DB 2; Length 557;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLLVAVGPWLVLSAAGGNLKSPOKVEVDIIDDNFIILWNRSDESQVNT 60  
 Db |||||  
 1 MMVLLGATTLLVAVGPWLVLSAAGGNLKSPOKVEVDIIDDNFIILWNRSDESQVNT 60  
 QY 61 FSPDYQKTMGNWIKLSCQNITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
 Db |||||  
 61 FSPDYQKTMGNWIKLSCQNITSTKCNFSSILKNVYEEIKLIRAEKENTSSWYEVDSF 120  
 QY 121 TPFRAQIIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
 Db |||||  
 121 TPFRAQIIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
 QY 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
 Db |||||  
 181 ENIYSRHKIYKLSPEPTYCLVKAAALLTSWKIGVYSPVHCITKTVENELPPENIEVSQ 240  
 QY 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 Db |||||  
 241 NQNYLKWDTYANMTFOVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 QY 301 GYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 Db |||||  
 301 GYLLRVQASDGNNTSFWSSEIKFDEIQAFLLPPVFNIRSLSDSFHHYIGAPKQSGNTP 360  
 QY 361 VTQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTVYCVKARAHMTDEKLNKSSV 420  
 Db |||||  
 361 VTQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTVYCVKARAHMTDEKLNKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db |||||  
 421 FSDAVCEKTKPGNTSK 436

## RESULT 9

AAR42635  
 ID AAR42635 standard; protein; 557 AA.

XX AAR42635;  
 AC

XX 25-MAR-2003 (revised)  
 DT 20-APR-1994 (first entry)

XX Human interferon receptor.  
 DE

XX IFN-R; extracellular domain; monoclonal antibody; viral infection;  
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;  
 KW psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;  
 KW immunodeficiency; measles virus; interferon-alpha-beta.  
 KW

XX Homo sapiens.  
 OS

XX Key Location/Qualifiers  
 FH Domain 1. 436

FT /label= extracellular\_domain  
 FT /note= "soluble, immunogenic form of IFN-R"

XX EP563487-A1.  
 PN

XX 06-OCT-1993.  
 PD

XX 31-MAR-1992; 92EP-00400902.  
 PF

XX 31-MAR-1992; 92EP-00400902.  
 PR

XX (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 PA

XX Benoit P, Meyer F, Meguire D, Plavec I, Tovey MG;  
 PI WPI; 1993-312951/40.  
 DR P-PSDB; AAR42635.

XX Monoclonal antibody to human interferon type-I receptor - having

PT neutralising activity against human type I interferon, used for therapy  
PT and diagnosis.  
XX Disclosure; Fig 3; 21pp; English.  
PS Monoclonal antibodies produced against soluble forms of the human  
CC interferon alpha-beta receptor based on the full-length human IFN-R  
CC sequence are claimed. The antibodies are useful for treatment and  
CC prophylaxis of disorders involving cell proliferation and/or viral  
CC infection. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2313; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVLVAGPWLVAAGGKLNKSPQKVEVDIIDDNFI LRNRSDS VGNVT 60  
Db 1 MMVLLGATTLVLVAGPWLVAAGGKLNKSPQKVEVDIIDDNFI LRNRSDS VGNVT 60  
QY 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLLWKNSSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLLWKNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
QY 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
RESULT 10  
ID ABU05091 standard; protein; 557 AA.  
XX  
AC ABU05091;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #1757.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200278524-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 28-MAR-2002; 2002WO-US0009671.

XX 28-MAR-2001; 2001US-0279495P.  
PR 21-MAY-2001; 2001US-0292544P.  
PR 08-AUG-2001; 2001US-0310801P.  
PR 01-OCT-2001; 2001US-0326370P.  
PR 04-DEC-2001; 2001US-0336780P.  
PR 20-FEB-2002; 2002US-0359985P.  
XX (ZYCO-) ZYCOS INC.  
PA Chiciz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
PS Example 2; SEQ ID NO 1757; 134pp; English.  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2313; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVLVAGPWLVAAGGKLNKSPQKVEVDIIDDNFI LRNRSDS VGNVT 60  
Db 1 MMVLLGATTLVLVAGPWLVAAGGKLNKSPQKVEVDIIDDNFI LRNRSDS VGNVT 60  
QY 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWEVDSF 120  
Db 61 FSDYQKTGMNDWIKLSGQCNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWEVDSF 120  
QY 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLLWKNSSGVEERI 180  
Db 121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLLWKNSSGVEERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVSPVHCITVTVENELPPENIEVSQ 240  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFOK 300  
QY 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWSEEEKFDTETIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVPNLKPLTVYCVKARAHMTDEKLNKSSV 420

```

QY 421 FSDAVCEKTPGNTSK 436
Db 421 FSDAVCEKTPGNTSK 436

RESULT 11
ABU05094
ID ABU05094 standard; protein; 557 AA.
AC ABU05094;
XX
XX
XX 29-JAN-2003 (first entry)
DT
DE Human expressed protein tag (EPT) #1760.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
FN
PD 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOS INC.
PA
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1760; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 6; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e-199;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
cytoskeletal proteins, receptors or transcription factors), useful for
treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
leukaemia.

```



PT leukemia.  
 XX Example 2; SEQ ID NO 1773; 134pp; English.  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 557 AA;  
 SQ

Query Match 100.0%; Score 2313; DB 6; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNDSVGNVT 60  
 DB 1 MMVLLGATTLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNDSVGNVT 60

QY 61 PSFDYQKTGMNDWIKLSCQNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120  
 DB 61 PSFDYQKTGMNDWIKLSCQNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120

QY 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180

QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITVTENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITVTENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFFQWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300  
 DB 241 NQNYVLKWDYTYANMTFFQWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300

QY 301 GYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKSGNTP 360  
 DB 301 GYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKSGNTP 360

QY 361 VTQDYPLIYEIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
 DB 361 VTQDYPLIYEIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436  
 DB 421 FSDAVCEKTKPGNTSK 436

RESULT 13  
 ABU05099  
 ID ABU05099 standard; protein; 557 AA.  
 XX AC ABU05099;  
 XX DT 29-JAN-2003 (first entry)  
 XX DE Human expressed protein tag (EPT) #1765.  
 XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.  
 XX Homo sapiens.  
 XX WO200278524-A2.  
 XX 10-OCT-2002.  
 XX 28-MAR-2002; 2002WO-US009671.  
 XX 28-MAR-2001; 2001US-0279495P.  
 XX 21-MAY-2001; 2001US-0292544P.  
 XX 08-AUG-2001; 2001US-0310801P.  
 XX 01-OCT-2001; 2001US-0326370P.  
 XX 04-DEC-2001; 2001US-0336780P.  
 XX 20-FEB-2002; 2002US-0358985P.  
 XX (ZYCO-) ZYCOS INC.  
 XX Chicx RM, Tomlinson AJ, Urban RG;  
 XX WPI; 2003-040607/03.  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX Example 2; SEQ ID NO 1765; 134pp; English.  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 557 AA;  
 SQ

Query Match 100.0%; Score 2313; DB 6; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNDSVGNVT 60  
 DB 1 MMVLLGATTLVAVGPWVLSAAGGKNLSPQKVEVDIIDNFIILNRNDSVGNVT 60

QY 61 PSFDYQKTGMNDWIKLSCQNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120  
 DB 61 PSFDYQKTGMNDWIKLSCQNITSTKCNFSSLLKLVYBEIKLIRAEKENTSSWYEDSF 120

QY 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180  
 DB 121 TPFRAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180

QY 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITVTENELPPENIEVSQ 240  
 DB 181 ENIYSRHKIYKLSPEPTYCLKVKAAALLTSWKIGVSPVHCITVTENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFFQWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300  
 DB 241 NQNYVLKWDYTYANMTFFQWLHAFKRNPGNHLKWKQIIPDCENVKTTQCVPQNVFQK 300

QY 301 GYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKSGNTP 360  
 DB 301 GYLLRVQASDGNNTSFWSSEIKFDTETIQAFLLPPVFNIRSLSDSFHYIGAPKSGNTP 360

QY 361 VTQDYPLIYEIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420  
 DB 361 VTQDYPLIYEIIFWNTSNAERKIEKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436  
 DB 421 FSDAVCEKTKPGNTSK 436

Db 241 NQNYLKWDTYANNTFQVWLHAFKRNPGNHLKWKQIPDCENVKTKQCVFPQNVFQK 300  
QY 301 GYLLRVQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTYVCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTYVCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436  
RESULT 14  
ID ABU05106  
XX ABU05106 standard; protein; 557 AA.  
AC ABU05106;  
XX  
XX  
XX 29-JAN-2003 (first entry)  
XX Human expressed protein tag (EPT) #1772.  
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
XX Homo sapiens.  
XX WO200278524-A2.  
XX 10-OCT-2002.  
XX 28-MAR-2002; 2002WO-US009671.  
XX 28-MAR-2001; 2001US-0279495P.  
XX 21-MAY-2001; 2001US-0292544P.  
XX 08-AUG-2001; 2001US-0310801P.  
XX 01-OCT-2001; 2001US-0326370P.  
XX 04-DEC-2001; 2001US-0336780P.  
XX 20-FEB-2002; 2002US-0358985P.  
XX (ZYCO-) ZYCOS INC.  
XX  
XX Chicz RM, Tomlinson AJ, Urban RG;  
XX WPI; 2003-040607/03.  
XX  
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX Example 2; SEQ ID NO 1772; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an

CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
Query Match 100.0%; Score 2313; DB 6; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLLVAVGFWLSSAAAGGKNLSPQKVEVDIIDDNFIILWNRSDSVGNVT 60  
Db 1 MMVLLGATTLLVAVGFWLSSAAAGGKNLSPQKVEVDIIDDNFIILWNRSDSVGNVT 60  
QY 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSILKLVYEEIKLIRAEKENTSSWTEVDSF 120  
Db 61 FSDYQKTGMNDNWKLSGCONITSTKCNFSSILKLVYEEIKLIRAEKENTSSWTEVDSF 120  
QY 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
Db 121 TPFKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERI 180  
QY 181 ENIYSRHKIYKLSPETTYCLVKQAALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240  
Db 181 ENIYSRHKIYKLSPETTYCLVKQAALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240  
QY 241 NQNYLKWDTYANNTFQVWLHAFKRNPGNHLKWKQIPDCENVKTKQCVFPQNVFQK 300  
Db 241 NQNYLKWDTYANNTFQVWLHAFKRNPGNHLKWKQIPDCENVKTKQCVFPQNVFQK 300  
QY 301 GYLLRVQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
Db 301 GYLLRVQASDGNNTSFWSEIEKFDTEIQAFLLPPVFNIRSLSDSFHYIYIGAPKQSGNTP 360  
QY 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTYVCVKARAHMTDEKLNKSSV 420  
Db 361 VIQDYPLIYEIIFWNTSNAERKIIIEKTDVTPNLPKPLTYVCVKARAHMTDEKLNKSSV 420  
QY 421 FSDAVCEKTKPGNTSK 436  
Db 421 FSDAVCEKTKPGNTSK 436  
RESULT 15  
ID ABU05097  
XX ABU05097 standard; protein; 557 AA.  
XX  
XX AC ABU05097;  
XX  
XX DT 29-JAN-2003 (first entry)  
XX  
XX DE Human expressed protein tag (EPT) #1763.  
XX  
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200278524-A2.  
XX  
XX PD 10-OCT-2002.  
XX  
XX PF 28-MAR-2002; 2002WO-US009671.  
XX  
XX PR 28-MAR-2001; 2001US-0279495P.  
XX PR 21-MAY-2001; 2001US-0292544P.  
XX PR 08-AUG-2001; 2001US-0310801P.  
XX PR 01-OCT-2001; 2001US-0326370P.  
XX PR 04-DEC-2001; 2001US-0336780P.  
XX PR 20-FEB-2002; 2002US-0358985P.  
XX  
XX PA (ZYCO-) ZYCOS INC.  
XX  
XX PI Chicz RM, Tomlinson AJ, Urban RG;  
XX  
XX DR WPI; 2003-040607/03.  
XX  
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.  
XX  
XX PS Example 2; SEQ ID NO 1772; 134pp; English.  
XX  
XX The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an

```
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
PA Chiciz RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX Human expressed protein tag (EPT) #1759.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
PT protease; protease inhibitor; transporter; cytoskeletal protein;
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 1763; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 6; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e-199;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGVPWVLSAAAGGKGLKSPQKVEVDIIDDNFILRNRSDES VGNVT 60
Db 1 MMVLLGATTLVLVAVGVPWVLSAAAGGKGLKSPQKVEVDIIDDNFILRNRSDES VGNVT 60

QY 61 FSDYQKTGMNDWNKLSGCQNTSTKCNFSSLLKLVYBEIKLIRAEKNTSSWYEDSF 120
Db 61 FSDYQKTGMNDWNKLSGCQNTSTKCNFSSLLKLVYBEIKLIRAEKNTSSWYEDSF 120

QY 121 TPFRAQIGPPEVHLEAEKALVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
Db 121 TPFRAQIGPPEVHLEAEKALVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180

QY 181 ENIYSRHKIYKLSPEYTCYCLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240
Db 181 ENIYSRHKIYKLSPEYTCYCLKVAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240

QY 241 NQNYVLKWDYTYANMTFQVWLHAFILKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300
Db 241 NQNYVLKWDYTYANMTFQVWLHAFILKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300

QY 301 GYLLLRVQASDGNNTSFWSSEIKFDEIQAFLILPPVFNIRSLSDSPHIYIGAPKQSGNTP 360
Db 301 GYLLLRVQASDGNNTSFWSSEIKFDEIQAFLILPPVFNIRSLSDSPHIYIGAPKQSGNTP 360

QY 361 VIQDYLPIIYEIIFWNTSNAERKIEBKTDVTVPNLKPLTYVCVKAHMTDEKLNKSSV 420
Db 361 VIQDYLPIIYEIIFWNTSNAERKIEBKTDVTVPNLKPLTYVCVKAHMTDEKLNKSSV 420

QY 421 FSDAVCEKTKPGNTSK 436
Db 421 FSDAVCEKTKPGNTSK 436

RESULT 16
```

```
ABU05093
ID ABU05093 standard; protein; 557 AA.
XX AC ABU05093;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1759.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX XX 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0328370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chiciz RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX PS Example 2; SEQ ID NO 1759; 134pp; English.
XX XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 6; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e-199;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLVLVAVGVPWVLSAAAGGKGLKSPQKVEVDIIDDNFILRNRSDES VGNVT 60
Db 1 MMVLLGATTLVLVAVGVPWVLSAAAGGKGLKSPQKVEVDIIDDNFILRNRSDES VGNVT 60

QY 61 FSDYQKTGMNDWNKLSGCQNTSTKCNFSSLLKLVYBEIKLIRAEKNTSSWYEDSF 120
Db 61 FSDYQKTGMNDWNKLSGCQNTSTKCNFSSLLKLVYBEIKLIRAEKNTSSWYEDSF 120
```

Db 61 FSDYQKTGMNDWNKLSGQCNITSTKCNFSSKLNVYBEIKLIRAEKENTSSWYEVDSF 120  
 QY 121 TPFRAQIGPPVHLEAEAKAIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGSGVEERI 180  
 Db 121 TPFRAQIGPPVHLEAEAKAIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEYTYCLVKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 Db 181 ENIYSRHKIYKLSPEYTYCLVKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 QY 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPPVFNIRSLDSFHYIYGAPKQSGNTP 360  
 Db 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPPVFNIRSLDSFHYIYGAPKQSGNTP 360  
 QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLKSSV 420  
 Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 17

ID ABU05100  
 XX ABU05100; standard; protein; 557 AA.  
 AC ABU05100;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX Human expressed protein tag (EPT) #1766.  
 DE  
 XX  
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX Homo sapiens.  
 XX  
 FN WO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 28-MAR-2002; 2002WO-US009671.  
 XX  
 PR 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 PA (ZYCO-) ZYCOS INC.  
 XX  
 XX Chicx RM, Tomlinson AJ, Urban RG;  
 PI  
 XX  
 DR WPI; 2003-040607/03.  
 XX  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 XX  
 XX Example 2; SEQ ID NO 1766; 134pp; English.  
 PS  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC

CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to this  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 557 AA;

Query Match 100.0%; Score 2313; DB 6; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1e-199;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLLGATTLLVAVGPVLSAAAGGKNLSPQKVEVDIIDDNFIILWNRSDESQVNT 60  
 Db 1 MMVLLGATTLLVAVGPVLSAAAGGKNLSPQKVEVDIIDDNFIILWNRSDESQVNT 60  
 QY 61 FSDYQKTGMNDWNKLSGQCNITSTKCNFSSKLNVYBEIKLIRAEKENTSSWYEVDSF 120  
 Db 61 FSDYQKTGMNDWNKLSGQCNITSTKCNFSSKLNVYBEIKLIRAEKENTSSWYEVDSF 120  
 QY 121 TPFRAQIGPPVHLEAEAKAIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGSGVEERI 180  
 Db 121 TPFRAQIGPPVHLEAEAKAIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGSGVEERI 180  
 QY 181 ENIYSRHKIYKLSPEYTYCLVKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 Db 181 ENIYSRHKIYKLSPEYTYCLVKVKAALLTSWKIGVSPVHCITKTVENELPPENIEVSQ 240  
 QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 Db 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQK 300  
 QY 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPPVFNIRSLDSFHYIYGAPKQSGNTP 360  
 Db 301 GIYLLRVQASDGNNTSFWSSEIKFDTETQAFLLPPVFNIRSLDSFHYIYGAPKQSGNTP 360  
 QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLKSSV 420  
 Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKKTDTVPNLKPLTVYCVKARAHMTWDEKLKSSV 420  
 QY 421 FSDAVCEKTKPGNTSK 436  
 Db 421 FSDAVCEKTKPGNTSK 436

## RESULT 18

ADR66319  
 ID ADR66319 standard; protein; 575 AA.  
 XX  
 AC ADR66319;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX Human prostatic carcinoma derived protein SEQ ID 173 #2.  
 DE human; cytostatic; diagnosis; prostatic cancer;  
 KW differential expression analysis.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004076614-A2.  
 XX  
 PD 10-SEP-2004.

XX PF 22-FEB-2004; 2004WO-DE000433.  
XX XX 27-FEB-2003; 2003DE-01009985.  
PR PR 14-MAY-2003; 2003DE-01022134.  
XX XX (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
XX (PILA/) PILARSKY C.  
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
PI Xinzhang L, Staub E;  
XX WPI; 2004-653386/63.  
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX Claim 2; Page 653; 1607pp; German.  
XX This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular  
CC weight below 5000, preferably 300, that binds to the polypeptide; an  
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
CC (monoclonal) antibody directed against Ab or any of the above derivatised  
CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
CC radioisotope. The polynucleotides are identified in human prostatic  
CC cancer by differential expression analysis, using DNA microarrays,  
CC between normal and tumorous tissues, with (over)expression being detected  
CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
CC prostatic cancer patients, or subjects at risk, were incubated  
CC sequentially with anti-human CD4 murine monoclonal antibodies;  
CC biotinylated second antibody; streptavidin-conjugated horseradish  
CC peroxidase and then diaminobenzidine as colour former (brown). The  
CC samples were counterstained with hemalum (blue). Malignant cells stained  
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
CC polynucleotide and polypeptide sequences used in the method of the  
CC invention.  
XX SQ Sequence 575 AA;  
Query Match 100.0%; Score 2313; DB 8; Length 575;  
Best Local Similarity 100.0%; Pred. No. 1.1e-199;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MMVLLGATTLVAVGPNVLSAAGKLNKSPQKVEVDIIDDNFTLRNRSDESIGNVT 60  
DB 19 MMVLLGATTLVAVGPNVLSAAGKLNKSPQKVEVDIIDDNFTLRNRSDESIGNVT 78  
QY 61 FSDYQKTMGNWIKLSCQNTTSTKCNFSSKLNVYBEIKLIRAEKENTSSWVEVSF 120  
DB 79 FSDYQKTMGNWIKLSCQNTTSTKCNFSSKLNVYBEIKLIRAEKENTSSWVEVSF 138  
QY 121 TPFRAQIGPPVHLEADKAIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGVEERI 180  
DB 139 TPFRAQIGPPVHLEADKAIVIHISPTKDSVMWALDGLSFTYSLLIWKNSGVEERI 198

QY 181 ENIYSRHKIYKLSPETTYCLKVKAAALTSWKIGVSPVHCIKTTVENELPPENIEVSQ 240  
DB 199 ENIYSRHKIYKLSPETTYCLKVKAAALTSWKIGVSPVHCIKTTVENELPPENIEVSQ 258  
QY 241 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPQNVFOK 300  
DB 259 NQNYVLKWDYTYANMTFQVWLHAFKRNPGNHLKWKQIPDCENVKTTQCVPQNVFOK 318  
QY 301 GIYLLRVQASDGNNTSFWSEEEKFTETQAFLLPPVFNIRSLSDSFHIGAPKQSGNTP 360  
DB 319 GIYLLRVQASDGNNTSFWSEEEKFTETQAFLLPPVFNIRSLSDSFHIGAPKQSGNTP 378  
QY 361 VTQDYPLIYEIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 420  
DB 379 VTQDYPLIYEIFWNTSNAERKIIIEKTDVTPNKLPLTVYCVKARAHMTDEKLNKSSV 438  
QY 421 FSDAVCEKTKPGNTSK 436  
DB 439 FSDAVCEKTKPGNTSK 454  
RESULT 19  
ADR66661  
ID ADR66661 standard; protein; 575 AA.  
XX  
AC ADR66661;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Human prostatic carcinoma derived protein SEQ ID 173 #3.  
XX human; cytostatic; diagnosis; prostatic cancer;  
KW differential expression analysis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004076614-A2.  
XX  
PD 10-SEP-2004.  
XX  
PF 22-FEB-2004; 2004WO-DE000433.  
XX  
PR 27-FEB-2003; 2003DE-01009985.  
PR 14-MAY-2003; 2003DE-01022134.  
XX (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
XX  
PI Hinzmamm B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;  
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;  
PI Xinzhang L, Staub E;  
XX  
DR WPI; 2004-653386/63.  
XX  
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,  
PT useful for diagnosis, treatment and in screening for specific binding  
PT agents.  
XX Claim 2; Page 1155; 1607pp; German.  
XX This invention describes novel cytostatic polynucleotide and polypeptide  
CC sequences which can be used in a method for diagnosing prostatic cancer  
CC or the risk of developing prostatic cancer. Diagnosis is based on  
CC determining over transcription or over expression of the sequences in  
CC prostatic tissue. Screening for inhibitors of the sequences or detection  
CC substances involves a binding assay, any compounds that bind are  
CC selected, optionally after deconvolution of mixtures. Detection of a  
CC predetermined minimum level of the reporter indicates the presence of  
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,  
CC short-interfering RNA or ribozymes; an organic molecule of molecular

CC weight below 5000, preferably 300, that binds to the polypeptide; an  
 CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the  
 CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human  
 CC (monoclonal) antibody directed against Ab or any of the above derivatised  
 CC with a reporter group, cell toxin, immunostimulatory molecules and/or  
 CC radioisotope. The polynucleotides are identified in human prostatic  
 CC cancer by differential expression analysis, using DNA microarrays,  
 CC between normal and tumorous tissues, with (over)expression being detected  
 CC by quantitative PCR. Analysis of prostatic cancer samples showed that  
 CC CD24 was upregulated in many of them. Sections of tissue, isolated from  
 CC prostatic cancer patients, or subjects at risk, were incubated  
 CC sequentially with anti-human CD4 murine monoclonal antibodies;  
 CC biotinylated second antibody; streptavidin-conjugated horseradish  
 CC peroxidase and then diaminobenzidine as colour former (brown). The  
 CC samples were counterstained with hemalum (blue). Malignant cells stained  
 CC strongly but non-malignant cells only weakly. In 15 of 63 samples of  
 CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and  
 CC lymph node metastases were also stained. ADR65805-ADR66954 represent the  
 CC polynucleotide and polypeptide sequences used in the method of the  
 CC invention.

XX  
 SQ Sequence 575 AA;

Query Match	100.0%;	Score 2313;	DB 8;	Length 575;
Best Local Similarity	100.0%;	Pred. No. 1.1e-199;		
Matches 436;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

QY	1	MMVLLGATTLVLVAGPWPVLSAAGGKNLKSFPQKVEVDIIDNFIILRNRSDESGVNT	60
Db	19	MMVLLGATTLVLVAGPWPVLSAAGGKNLKSFPQKVEVDIIDNFIILRNRSDESGVNT	78
QY	61	FSFDYQKTGMNWIKLSGQNTSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEVDSF	120
Db	79	FSFDYQKTGMNWIKLSGQNTSTKCNFSSILKLVYEEIKLIRAEKENTSSWYEVDSF	138
QY	121	TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVERI	180
Db	139	TPFRKAQIGPPEVHLEADKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVVERI	198
QY	181	ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPEIEVSQ	240
Db	199	ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPEIEVSQ	258
QY	241	NQNYVLKWDYTYANMTFQVWLHAFILKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK	300
Db	259	NQNYVLKWDYTYANMTFQVWLHAFILKRNPGNHLKYWKQIPDCENVKTTQCVFPQNVFQK	318
QY	301	GIYLLRVQASDCGNNTSPWSEETKEPTEIQAFLLPPVENIRSLSDSFHIYIGAPKQSGNTP	360
Db	319	GIYLLRVQASDCGNNTSPWSEETKEPTEIQAFLLPPVENIRSLSDSFHIYIGAPKQSGNTP	378
QY	361	VIQDYPLIYEIIFWNTSNAERKIEKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV	420
Db	379	VIQDYPLIYEIIFWNTSNAERKIEKKTDTVVPNLKPLTVYCVKARAHMTDEKLNKSSV	438
QY	421	FSDAVCEKTKPGNTSK	436
Db	439	FSDAVCEKTKPGNTSK	454

Search completed: January 18, 2006, 06:27:26  
 Job time : 137 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 07:06:01 ; Search time 112.108 Seconds  
(without alignments)  
2523.620 Million cell updates/sec

Title: US-10-824-981-2\_COPY\_27\_427  
Perfect score: 2141  
Sequence: 1 GKULKSPQKVEVDIIDNFI.....AHTMDEKLKSSVPSDAVCE 401

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05\_80.\*

1: uniprot\_sprot.\*

2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	100.0	557	INARI_HUMAN	P17181 homo sapien
2	2141	100.0	557	Q53H11_HUMAN	Q53H11 homo sapien
3	2134	99.7	557	Q53GW9_HUMAN	Q53GW9 homo sapien
4	1912	89.3	387	Q6PKD7_HUMAN	Q6PKD7 homo sapien
5	1663.5	77.7	477	Q4727_MACFA	Q4727 macaca fasc
6	1438	67.2	560	INARI_PIG	Q764M8 sus scrofa
7	1384.5	64.7	560	INARI_BOVIN	Q04790 bos taurus
8	1382.5	64.6	560	INARI_SHEEP	Q28589 ovis aries
9	1082	50.5	332	Q9GK86_SHEEP	Q9GK86 ovis aries
10	966	45.1	590	INARI_MOUSE	P33896 mus musculus
11	959	44.8	590	Q80UR8_MOUSE	Q80UR8 mus musculus
12	958	44.7	590	Q80UJ3_MOUSE	Q80UJ3 mus musculus
13	677.5	31.6	449	Q5X105_CHICK	Q5X105 gallus gall
14	677.5	31.6	569	Q5XP11_CHICK	Q5XP11 gallus gall
15	674.5	31.5	442	Q9PVJ9_CHICK	Q9PVJ9 gallus gall
16	668.5	31.2	569	Q9VHW0_CHICK	Q9VHW0 gallus gall
17	262.5	12.3	111	Q6LD20_MOUSE	Q6LD20 mus musculus
18	246	11.5	98	Q6LD22_MOUSE	Q6LD22 mus musculus
19	229	10.7	317	Q58CP3_BOVIN	Q58CP3 bos taurus
20	220	10.3	325	Q110R2_HUMAN	Q63934 mus sapien
21	220	10.3	327	Q6ZVU9_HUMAN	Q6ZVU9 homo sapien
22	216.5	10.1	349	Q110R2_MOUSE	Q61190 mus musculus
23	216.5	10.1	351	Q8VHM7_MOUSE	Q8VHM7 mus musculus
24	202.5	9.5	362	Q764M7_PIG	Q764M7 sus scrofa
25	199	9.3	332	Q78EC1_9MURI	Q78EC1 mus sp. int
26	199	9.3	332	Q63953_MOUSE	Q63953 mus musculus
27	196	9.2	334	Q5RL90_CHICK	Q5RL90 gallus gall
28	194.5	9.1	333	Q72T30_TETNG	Q72T30 tetraodon n
29	190	8.9	59	Q9GK85_SHEEP	Q9GK85 ovis aries
30	185	8.6	213	Q8C352_MOUSE	Q8C352 mus musculus
31	183.5	8.6	341	Q9YGC8_CHICK	Q9YGC8 gallus gall

RESULT 1

ID	INARI_HUMAN	STANDARD;	PRT;	557 AA.
AC	P17181; Q8WTZ2;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-FEB-2005 (Rel. 46, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).			
GN	Name=IFNARI; Synonyms=IFNAR;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
FN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=90124632; PubMed=2153461;			
RA	Uze G., Lutfalla G., Gresser I.;			
RT	"Genetic transfer of a functional human interferon alpha receptor into			
RT	mouse cells: cloning and expression of its cDNA."			
RL	Cell 60:225-234 (1990).			
RL	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=92129376; PubMed=1370833;			
RA	Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;			
RT	"The structure of the human interferon alpha/beta receptor gene."			
RL	J. Biol. Chem. 267:2802-2809 (1992).			
RL	[3]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-168; ILE-307 AND			
RP	MET-359.			
RA	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,			
RA	Rajkumar N., Yi Q., Nickerson D.A.;			
RT	"SeattlesNPs. NHLBI HL66682 program for genomic applications, UW-			
RT	FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
RL	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT VAL-168.			
RP	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pearce C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McSwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

ALIGNMENTS

RA Butterfield Y.S.N., Kraywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP PHOSPHORYLATION BY TYK2.  
RX MEDLINE=95059042; PubMed=7526154;  
RA Colamonicci O., Yan H., Domanski P., Handa R., Smalley D.,  
RA Mullersman J., Witte M., Krishnan K., Krolewski J.;  
RT "Direct binding to and tyrosine phosphorylation of the alpha subunit  
RT of the type I interferon receptor by p135tyk2 tyrosine kinase.";  
RL Mol. Cell. Biol. 14:8133-8142(1994).  
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
CC subunits themselves.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: IFN receptors are present in all tissues and  
CC even on the surface of most IFN-resistant cells.  
CC -!- PTM: Phosphorylated on tyrosine residues by TYK2 tyrosine kinase.  
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC -----  
CC EMBL; J03171; AAA52730.1; -; mRNA.  
CC EMBL; X60459; CAA42992.1; -; Genomic DNA.  
CC EMBL; AY654286; AAT49100.1; -; Genomic DNA.  
CC EMBL; BC021825; AA421825.1; -; mRNA.  
CC PIR; A32694; A32694.  
CC Ensembl; ENSG00000142166; Homo sapiens.  
CC HGNC; HGNC:5432; IFNARI.  
CC H-InvDB; HIX0016075; -.  
CC MIM; 107450; -.  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0004905; F:interferon-alpha/beta receptor activity; TAS.  
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
CC GO; GO:0007259; P:JAK-STAT cascade; TAS.  
CC GO; GO:0009615; P:response to virus; TAS.  
CC InterPro; IPR00282; Cytok receptor\_2.  
CC InterPro; IPR003961; FN III.  
CC PROSITE; PS00853; FN3; FALSE NEG.  
KW Glycoprotein; Phosphorylation; Polymorphism; Receptor; Repeat; Signal;  
KW Transmembrane.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 557 Interferon-alpha/beta receptor alpha  
FT chain.  
FT TOPO\_DOM 28 436 Extracellular (Potential).  
FT TRANSMEM 437 457 Potential.  
FT TOPO\_DOM 458 557 Cytoplasmic (Potential).  
FT DOMAIN 134 224 Fibronectin type-III 1.  
FT DOMAIN 230 326 Fibronectin type-III 2.  
FT DOMAIN 334 425 Fibronectin type-III 3.  
FT MOD\_RES 466 466 Phosphotyrosine (by TYK2) (Probable).  
FT MOD\_RES 481 481 Phosphotyrosine (by TYK2) (Probable).  
FT CARBOHYD 50 50 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 58 58 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 81 81 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 88 88 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 110 110 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 172 172 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 254 254 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 313 313 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 314 314 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 376 376 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 416 416 N-linked (GlcNAc. .) (Potential).  
FT CARBOHYD 433 433 N-linked (GlcNAc. .) (Potential).  
FT DISULFID 79 87 By similarity.

FT DISULFID 199 220 By similarity.  
FT VARIANT 168 168 L -> V.  
FT /FTID=VAR\_002717.  
FT VARIANT 307 307 V -> I.  
FT /FTID=VAR\_020502.  
FT VARIANT 359 359 T -> M.  
FT /FTID=VAR\_020503.  
FT CONFLICT 17 17 A -> G (in Ref. 1).  
FT SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75C8C CRC64;  
Query Match 100.0%; Score 2141; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 3.1e-154;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKNLKSPQKVEVDIIDDNFILRNWRSDSGVNTFSPDYOKTGMDNWKILSGCQNTITSTK 60  
DB 27 GKNLKSPQKVEVDIIDDNFILRNWRSDSGVNTFSPDYOKTGMDNWKILSGCQNTITSTK 86  
QY 61 CNFSSSLKLVNYYEIKLRIRAEKENTSSWEVDSTFPRKQAIQGPPEVHLEAEDKAIIVHI 120  
DB 87 CNFSSSLKLVNYYEIKLRIRAEKENTSSWEVDSTFPRKQAIQGPPEVHLEAEDKAIIVHI 146  
QY 121 SPQTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 180  
DB 147 SPQTKDSVMWALDGLSFTYSLLIWKNSGSGVEERIENIYSRHKIYKLSPETTYCLKVKAAAL 206  
QY 181 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNYLVKWDYTYANMTFOVOMLHAPL 240  
DB 207 LTSWKIGVSPVHCIKTTVENELPPENIEVSQNVQNYLVKWDYTYANMTFOVOMLHAPL 266  
QY 241 KRNPNGNHYKWKQIPDCENVKTTQCVPQNVFQKGYLLRVQASDGNNTSFWSSEIKFDT 300  
DB 267 KRNPNGNHYKWKQIPDCENVKTTQCVPQNVFQKGYLLRVQASDGNNTSFWSSEIKFDT 326  
QY 301 EIQAFLLPPVFNIRSLSDSFHIVIGAPKQSGNTPTVQDYPLIYEIIFWENTSNAERKIE 360  
DB 327 EIQAFLLPPVFNIRSLSDSFHIVIGAPKQSGNTPTVQDYPLIYEIIFWENTSNAERKIE 386  
QY 361 KKTDTVTPNKLKPLTVYCVKARAHTMDEKLNKSSVFSFDANCE 401  
DB 387 KKTDTVTPNKLKPLTVYCVKARAHTMDEKLNKSSVFSFDANCE 427  
RESULT 2  
Q53H11 HUMAN  
ID Q53H11\_HUMAN PRELIMINARY; PRT; 557 AA.  
AC Q53H11;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Interferon-alpha receptor 1 variant (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Maruyama K., Sugano S.;  
RT "Oligo-capping: a simple method to replace the cap structure of  
RT eucaryotic mRNAs with oligoribonucleotides.";  
RL Gene 138:171-174(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano S.;  
RT "Construction and characterization of a full length-enriched and a 5'-  
RT end-enriched cDNA library.";  
RL Gene 200:149-156(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;



RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,  
RA Tanaka A., Yokoyama S.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
KW EMBL; AK222770; BAD96490.1; -, mRNA.  
DR Receptor.  
FT NON TER  
SQ SEQUENCE 557 AA; 63539 MW; 3CC744C8A0A75CBC CRC64;  
Query Match 100.0%; Score 2141; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 3.1e-154;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GKNLSPQKVEVDIIDDNFILRWNRSDSGVNTFSFDYQKGTGMDNWKLSGCONITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRWNRSDSGVNTFSFDYQKGTGMDNWKLSGCONITSTK 86  
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEDVSTFPFRKAQIGPEVHLEAEDKAIVIH 120  
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEDVSTFPFRKAQIGPEVHLEAEDKAIVIH 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERENIYSRHKIYKLSPETTYCLKVKAAL 206  
Qy 191 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 266  
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTFSWSEIKPDT 300  
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTFSWSEIKPDT 326  
Qy 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYEIIFWENTSNAERKII 360  
Db 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYEIIFWENTSNAERKII 386  
Qy 361 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSDAVCE 427  
RESULT 3  
Q53GW9 HUMAN PRELIMINARY; PRT; 557 AA.  
AC Q53GW9;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Interferon-alpha receptor 1 variant (fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Maruyama K., Sugano S.;  
RT "Oligo-capping : a simple method to replace the cap structure of  
RT eucaryotic mRNAs with oligoribonucleotides.";  
RL Gene 138:171-174 (1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;  
RT "Construction and characterization of a full length-enriched and a 5'-  
RT end-enriched cDNA library.";  
RL Gene 200:149-156 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,  
RA Tanaka A., Yokoyama S.;

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK222812; BAD96532.1; -, mRNA.  
KW Receptor.  
FT NON TER  
SQ SEQUENCE 557 AA; 63598 MW; 2D9522BBCC775486 CRC64;  
Query Match 99.7%; Score 2134; DB 2; Length 557;  
Best Local Similarity 99.5%; Pred. No. 1.1e-153;  
Matches 399; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GKNLSPQKVEVDIIDDNFILRWNRSDSGVNTFSFDYQKGTGMDNWKLSGCONITSTK 60  
Db 27 GKNLSPQKVEVDIIDDNFILRWNRSDSGVNTFSFDYQKGTGMDNWKLSGCONITSTK 86  
Qy 61 CNFSSKLNVYEEIKLIRAEKENTSSWYEDVSTFPFRKAQIGPEVHLEAEDKAIVIH 120  
Db 87 CNFSSKLNVYEEIKLIRAEKENTSSWYEDVSTFPFRKAQIGPEVHLEAEDKAIVIH 146  
Qy 121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERENIYSRHKIYKLSPETTYCLKVKAAL 180  
Db 147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVBERENIYSRHKIYKLSPETTYCLKVKAAL 206  
Qy 191 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 240  
Db 207 LTSWKIGYSPVHCITKTVENELPPENIEVSQNVQNVLVKWDYTYANMTFQVQWLHAF 266  
Qy 241 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTFSWSEIKPDT 300  
Db 267 KRNPNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTFSWSEIKPDT 326  
Qy 301 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYEIIFWENTSNAERKII 360  
Db 327 EIQAFLLPPVFNIRSLSDSFHYIYGAPKQSGNTPIQDYPLIYEIIFWENTSNAERKII 386  
Qy 361 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSDAVCE 401  
Db 387 KKTDTVTNPKLTYVCVKARAHMTDEKLNKSSVFSDAVCE 427  
RESULT 4  
Q6PKD7 HUMAN PRELIMINARY; PRT; 387 AA.  
AC Q6PKD7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IFNAR1 protein (Fragment).  
CN Name=IFNAR1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RA Strauberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002590; AA02590.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR InterPro; IPR000282; Cytok_receptor_2.  
FT NON TER 387  
SQ SEQUENCE 387 AA; 44388 MW; DEC1A8CC2F44499 CRC64;  
  
Query Match 89.3%; Score 1912; DB 2; Length 387;  
Best Local Similarity 99.7%; Pred. No. 5e-137;  
Matches 356; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GKNLKSPQKVEVDIIDNFILRNWRSDES VGNVTFSPDYQKTGMNDWIKLSGCCQNIITSTK 60  
Db 27 GKNLKSPQKVEVDIIDNFILRNWRSDES VGNVTFSPDYQKTGMNDWIKLSGCCQNIITSTK 86  
  
Qy 61 CNFSSLLKLVNVEEIKLRIRAEKNTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 120  
Db 87 CNFSSLLKLVNVEEIKLRIRAEKNTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKAI VIHI 146  
  
Qy 121 SPGTKDSVMWALDGLSFTSYLLIWNKSSGVVEERIENIYSRHKIYKLSPETTYCLVKVAAL 180  
Db 147 SPGTKDSVMWALDGLSFTSYLLIWNKSSGVVEERIENIYSRHKIYKLSPETTYCLVKVAAL 206  
  
Qy 181 LTSWKIGVYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVOWLHAF 240  
Db 207 LTSWKIGVYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVOWLHAF 266  
  
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Qy 301 EIQAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPIQDYPLIYIIFWNTSNAERK 357  
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RESULT 5  
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AC Q4R727;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Testis cDNA, clone: QtaA-16508, similar to human interferon (alpha,  
DE beta and omega) receptor 1 (IPNARI), mRNA, RefSeq: NM_00629.2.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopitheidae; Cercopithecinae; Macaca.  
OX NCBI_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA International consortium for macaque cDNA sequencing, analysis;  
RT "DNA sequences of macaque genes expressed in brain or testis and its  
RL evolutionary implications";  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,  
RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;  
RT "Substitution rate and structural divergence of 5'UTR evolution:  
RT Comparative analysis between human and cynomolgus monkey cDNAs";  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
```

```
DR EMBL; AB169002; BAB01097.1; -; mRNA.  
DR InterPro; IPR000282; Cytok_receptor_2.  
KW Receptor; Transmembrane.  
SQ SEQUENCE 477 AA; 54766 MW; 1D4110D471060BCF CRC64;  
  
Query Match 77.7%; Score 1663.5; DB 2; Length 477;  
Best Local Similarity 91.1%; Pred. No. 5.3e-118;  
Matches 316; Conservative 10; Mismatches 20; Indels 1; Gaps 1;  
  
Qy 56 ITSTKCNFSSLLKLVNVEEIKLRIRAEKNTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKA 115  
Db 1 MTSTKCNFSSLLKLVNVEEIKLRIRAEKNTSSWYEVDSFTPPRKAQIGPPEVHLEAEDKA 60  
  
Qy 116 IVIHIS-PGTKDSVMWALDGLSFTSYLLIWNKSSGVVEERIENIYSRHKIYKLSPETTYCL 174  
Db 61 IVIYISPPGTTSDSVWALDRSSFTSYLLIWNKSSGVVEERIENIYSRHKIYKLSPETTYCL 120  
  
Qy 175 KVKAALLTSMKIGVYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVQ 234  
Db 121 KVKAALLTSRKIGVYSPVHCITKTVENELPPENIEVSVQNVYLVKWDVTYANMTFQVQ 180  
  
Qy 235 WLHAFLLKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWS E 294  
Db 181 WLHAFLLKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWS E 240  
  
Qy 295 EIKFDTETIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPIQDYPLIYIIFWNTSNA 354  
Db 241 EIKFDTETIOAFLPPVFNIRSLSDSFHYIYGAPKQSGNTVPIQDYPLIYIIFWNTSNA 300  
  
Qy 355 ERKIIKKKTDVTVPNLKPLTVYCVKARAHMTDMLKNSKSSVFS DAVCE 401  
Db 301 ERKIIKKKTDVTVPNLKPLTVYCVKARAHMTDMLKNSKSSVFS DAVCE 347  
  
RESULT 6  
INARI_PIG  
ID INARI_PIG STANDARD; PRT; 560 AA.  
AC Q764M6;  
DT 10-MAY-2005 (Rel. 47, Created)  
DT 10-MAY-2005 (Rel. 47, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
GN Name=IFNARI;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX PubMed=14681463; DOI=10.1093/nar/gkh037;  
RA Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H.,  
RA Okumura N., Hamasima N., Awata T.;  
RT "PEDE (Pig EST Data Explorer): construction of a database for ESTs  
RL derived from porcine full-length cDNA libraries.";  
RL Nucleic Acids Res. 32:D484-D488(2004).  
CC -!- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
CC subunits themselves (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the type II cytokine receptor family.  
CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; AB116561; BAD06315.1; -; mRNA.  
DR InterPro; IPR000282; Cytok_receptor_2.  
DR InterPro; IPR003961; FN_III.
```

DR PROSITE, PS50853; FN3; FALSE\_NEG  
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24 By similarity.  
 FT CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.  
 FT TOPO\_DOM 25 437 Extracellular (Potential).  
 FT TRANSMEM 438 458 Potential.  
 FT TOPO\_DOM 459 560 Cytoplasmic (Potential).  
 FT DOMAIN 133 224 Fibronectin type-III 1.  
 FT DOMAIN 230 326 Fibronectin type-III 2.  
 FT DOMAIN 334 426 Fibronectin type-III 3.  
 FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 222 222 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 249 249 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 76 84 By similarity.  
 FT DISULFID 199 220 By similarity.  
 SQ SEQUENCE 560 AA; 63221 MW; DC193651033DFBDB CRC64;

Query Match 67.2%; Score 1438; DB 1; Length 560;  
 Best Local Similarity 66.4%; Pred. No. 9.3e-101;  
 Matches 269; Conservative 63; Mismatches 69; Indels 4; Gaps 4;

QY 1 GNKLSPQKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTDGMDNWLKSGCNITSTK 60  
 DB 24 GADLRSPNVVSIIDDNFILRWNRSDSVGNVTFSDYQKTDGMDNWLKSGCNITSTK 83  
 QY 61 CNFSSKLK-NVYEIKLIRAEKEN-TSSWEVDSTFPFKAQIGPPVHLEAEDKAIVI 118  
 DB 84 CNFSSIKLVYEKTKLIRAEKNGSTSPWYEVFPFQEAQIGPPDVHLEAEDKAI 143  
 QY 119 HIS-PGTKDSVMWALDGLSFYSLLIWNKSSGVEERIENIYSRHKYKLSPEITCLVK 177  
 DB 144 NLSPGPTKNSVMWAMDSSSFYSLVIWNKSSLEERTKTVDYARDKIHLSPETTYCLVK 203  
 QY 178 AALLTSWIKGVSPVHCITTVENELPPENIEVSQNVYLVKWDYTYANNFTQVOWLH 237  
 DB 204 AGLRSPKGVSPVSPYICITTVTKHLPSPENLEINAEVRVYLVKNYTYENVTFQAQWLH 263  
 QY 238 AFLKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFKGILYLRVQASDGNNTSPWSEIK 297  
 DB 264 AFLKKIPEDHSDKWKQIPCNENKTHCVFPQNVTKGIFPIRVQASNGNSTLSSEKR 323  
 QY 298 FDTETQAFLLPVPFNIRSLD-SFHYIYGAPKQSGNTPTVIDYPLIYIIFWENTSNAER 356  
 DB 324 FNTENQTLFPVIVNKPINDASLRVGIGAPKSESDKSNQLYPLIYEVIPRENTSDTER 383  
 QY 357 KLIKKTDTVPLNPLTYCVKARAHWTDEKLNKSSVFSDAVCE 401  
 DB 384 DVLEKRTDTFTSNLPLTYCVKARALIENDRNWRSSVFSDTVCE 428

## RESULT 7

INARI\_BOVIN STANDARD; PRT; 560 AA.  
 AC Q04790;  
 DT 01-FEB-1993 (Rel. 27, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).  
 GN Name=IFNARI; Synonyms=IFNAR;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=93076908; PubMed=1446745; DOI=10.1016/0014-5793(92)81204-Y;  
 RA Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;  
 RT "Specific antiviral activities of the human alpha interferons are  
 determined at the level of receptor (IFNAR) structure.";  
 RL FEBS Lett. 313:255-259(1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93305725; PubMed=8318540; DOI=10.1016/0167-4781(93)90129-2;  
 RA Lim J.-K., Langer J.A.;  
 RT "Cloning and characterization of a bovine alpha interferon receptor.";  
 RL Biochim. Biophys. Acta 1173:314-319(1993).  
 CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
 I IFNs triggers tyrosine phosphorylation of a number of proteins  
 including JAKs, TYK2, STAT proteins and IFNAR alpha- and beta-  
 subunits themselves.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL; X68443; CAA48484.1; -; mRNA.  
 DR EMBL; L06320; AAA02571.1; -; mRNA.  
 DR PIR; S27387; S27387.  
 DR InterPro; IPR000282; Cytok receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR001187; Tissue\_factor.  
 DR Pfam; PF01108; Tissue\_fac; 1.  
 DR PROSITE; PS50853; FN3; 2.  
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24 By similarity.  
 FT CHAIN 25 560 Interferon-alpha/beta receptor alpha chain.  
 FT TOPO\_DOM 25 437 Extracellular (Potential).  
 FT TRANSMEM 438 458 Potential.  
 FT TOPO\_DOM 459 560 Cytoplasmic (Potential).  
 FT DOMAIN 133 224 Fibronectin type-III 1.  
 FT DOMAIN 230 326 Fibronectin type-III 2.  
 FT DOMAIN 334 426 Fibronectin type-III 3.  
 FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 254 254 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 76 84 By similarity.  
 FT DISULFID 199 220 By similarity.  
 FT CONFLICT 422 422 F -> V (in Ref. 2).  
 SQ SEQUENCE 560 AA; 63819 MW; 66D76B72861B1D11 CRC64;

Query Match 64.7%; Score 1384.5; DB 1; Length 560;  
 Best Local Similarity 64.0%; Pred. No. 1.1e-96;  
 Matches 258; Conservative 62; Mismatches 78; Indels 5; Gaps 5;

QY 3 NLKSPQKVEVDIIDDNFILRWNRSDSVGNVTFSDYQKTDGMDNWLKSGCNITSTKCN 62  
 DB 27 NLK-PENVEIHIDNDFLKNSSSVGNVTFSDYQKTDGMDNWLKSGCNITSTKCN 85  
 QY 63 FSSKLK-NVYEIKLIRAEK-ENTSSWYVDSTFPFKAQIGPPVHLEAEDKAIVTHI 120  
 DB 86 FSSVELENVFEKILIRAEKNGNSTTWYEVFPFPEAIGPPDVHLEAEDKAIILSI 145  
 QY 121 S-PGTKDSVMWALDGLSFYSLLIWNKSSGVEERIENIYSRHKYKLSPEITCLVKAA 179

Db 146 SPPTGDSIMWMDRSSFRYSVWIKNSSLSLEERTETVYPBCKIYKLSPEITYCLKVKAE 205  
 Qy 180 LLTSWKIGVSPVHCITKTVENLPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 239  
 Db 206 LRQSRVGCYSPVCINTTEHKVPSENIQADNQIYVLKWDYTYANMTFQVQWLHAF 265  
 Qy 240 LKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEEEKFD 299  
 Db 266 FKIPGNHSDKWKQIPNCENVTSTHCVPFREVSRGGIYVVRASNGNGTSFWSEEEKFN 325  
 Qy 300 TEIQAFLLPPVFNIRSL-DSFHYIGAPKQSGNTVPVIQDPLIYELIFWENTSNAERKI 358  
 Db 326 TEMKTIIPFPVISMKSITDLSLHVSASESESNMNSQYPLIYELIFWENTSNAERKV 385  
 Qy 359 IEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401  
 Db 386 LEKRTDFTFNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 428

RESULT 8  
 INARI SHEEP STANDARD; PRT; 560 AA.  
 AC Q28585; Q95206; PRT; 560 AA.  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)  
 DE (Interferon alpha/beta receptor-1).  
 GN Name=IFNAR1; Synonyms=IFNAR;  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Ovis.  
 OC NCBI\_TaxID=9940;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Endometrium;  
 RX MEDLINE=97135690; PubMed=8981227; DOI=10.1677/jme.0.0170207;  
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;  
 RT "Structure of an ovine interferon receptor and its expression in  
 endometrium.";  
 RL J. Mol. Endocrinol. 17:207-215 (1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Endometrium;  
 RX MEDLINE=98008426; PubMed=9348203; DOI=10.1210/en.138.11.4757;  
 RA Han C.-S., Mathiasdan N., Klemann S.W., Roberts R.M.;  
 RT "Molecular cloning of ovine and bovine type I interferon receptor  
 subunits from uteri, and endometrial expression of messenger  
 ribonucleic acid for ovine receptors during the estrous cycle and  
 pregnancy.";  
 RL Endocrinology 138:4757-4767 (1997).  
 CC -1- FUNCTION: Receptor for interferons alpha and beta. Binding to type  
 CC I IFNs triggers tyrosine phosphorylation of a number of proteins  
 CC including JAKs, TYK2, STAT proteins and IFN alpha- and beta-  
 CC subunits themselves.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined except  
 CC conceptus at day 15 of pregnancy.  
 CC -1- SIMILARITY: Belongs to the type II cytokine receptor family.  
 CC -1- SIMILARITY: Contains 3 fibronectin type-III domains.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X95939; CAA65183.1; -; mRNA.  
 CC EMBL; U65978; AAB84231.1; -; mRNA.  
 DR InterPro; IPR000282; Cytok\_receptor\_2.  
 DR InterPro; IPR003961; FN\_III.  
 DR PROSITE; PS50853; FN3; 3.

KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 24 By similarity.  
 FT FT 25 560 Interferon-alpha/beta receptor alpha  
 FT chain.  
 FT FT 25 560 Extracellular (Potential).  
 FT TOPO\_DOM 25 437 Potential.  
 FT TRANSMEM 438 458 Cytoplasmic (Potential).  
 FT TOPO\_DOM 459 560 Fibronectin type-III 1.  
 FT DOMAIN 125 224 Fibronectin type-III 2.  
 FT DOMAIN 230 326 Fibronectin type-III 3.  
 FT DOMAIN 330 426  
 FT CARBOHYD 47 47 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 108 108 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 109 109 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 222 222 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 285 285 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 313 313 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 359 359 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 377 377 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 76 84 By similarity.  
 FT DISULFID 199 220 By similarity.  
 FT CONFLICT 352 352 S -> G (in Ref. 2).  
 FT CONFLICT 522 522 A -> D (in Ref. 2).  
 SQ SEQUENCE 560 AA; E7198A1905D4805C CRC64;

Query Match 64.8%; Score 1382.5; DB 1; Length 560;  
 Best Local Similarity 63.5%; Pred. No. 1.5e-96;  
 Matches 256; Conservative 65; Mismatches 77; Indels 5; Gaps 5;

Qy 3 NLKSPQKVEVDIIDDNFILRWNSDESQVGNVTFSPDYQKGTGMDNWIKSGQNTITSKCN 62  
 Db 27 NLKS-ENVEIHIIDDNFILRWNSDESQVGNVTFSPDYQKGTGMDNWIKSGQNTITSKCN 85  
 Qy 63 FSSILKL-NVYEEIKLRIRAEK-ENTSSWYEVDSFTPRKQIIGPPEVHLBAEDKAIYIHI 120  
 Db 86 FSSVELKQVFEKIELIRAEK-ENTSSWYEVDSFTPRKQIIGPPEVHLBAEDKAIYIHI 145  
 Qy 121 S-PGTQDSVMWALDGLSFTYSLIWNKSSGVERIENIYSRHKIYKLSPEITYCLKVKAA 179  
 Db 146 SPFGTDSIMWALDRSSFRYSVWIKNSSLSLEERTETVYPBCKIYKLSPEITYCLKVKAE 205  
 Qy 180 LLTSWKIGVSPVHCITKTVENLPPENIEVSVQONQYVLKWDYTYANMTFQVQWLHAF 239  
 Db 206 LRQSRVGCYSPVCINTTEHKVPSENIQADNQIYVLKWDYTYANMTFQVQWLHAF 265  
 Qy 240 LKRNPGNHLKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSPWSEEEKFD 299  
 Db 266 FKIPGNHSDKWKQIPNCENVTSTHCVPFREVSRGGIYVVRASNGNGTSFWSEEEKFN 325  
 Qy 300 TEIQAFLLPPVFNIRSL-DSFHYIGAPKQSGNTVPVIQDPLIYELIFWENTSNAERKI 358  
 Db 326 TEMKTIIPFPVISMKSITDLSLHVSASESESNMNSQYPLIYELIFWENTSNAERKV 385  
 Qy 359 IEKKTDTVPNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 401  
 Db 386 LEKRTDFTFNLKPLTVYCVKARAHMTDEKLNKSSVFSDAVCE 428

RESULT 9  
 Q9GK86 SHEEP PRELIMINARY; PRT; 332 AA.  
 AC Q9GK86;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Type I interferon receptor 1e.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Ovis.







```
Db 90 HTECDFSSAITAYDYTHIRAEERREAKSPWISFEMIPYEIAQIGPPEIALQSGINGAI 149
Qy 117 VIHISPTKDSV--MWALDGLSFTYSLIIWKNSSGVEERIENIYSRHKIYKLSPEPTYCL 174
Db 150 KINISPPANQVRKMW-LISVFFKYNVIVDWSNSV-EKVRSLIPDIVINDLAPETTYCL 207
Qy 175 KVKAAALTSWKIGVSPVHCIKTTVE--NELPPPENIEVSVQNQNYVLKWDYTY--ANMTFQ 232
Db 208 KVQATVPLEDKGLFSPHICIKITRKVNDLLCPTNVRVFPALNMKFYLLWHDNHNHVEHYTYT 267
Qy 233 VQWLHAPLKRNPNGNHLKWKQIPDCENVKTTQC-----VFPQNVFQKGIYLLRVQASDGN 287
Db 268 VQYLTGVLKMLYDDYSKWQKVSVCENITSMKCNLSVVIKPTS----ASYFFRVQAMNEY 323
Qy 288 NTSFMSSEIKFDPTEIOAFLLPPVFNIRSLSDSHIYIGAPKQSGNTPIQDYPILYELIF 347
Db 324 NKSLSKDVEVDPVVTNEIGPPDVKVDISDVLHLHIKITPPGPGNKIMSLDLYDFPYQILY 383
Qy 348 WENTSNAERKIIIEKKTDD--VTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVC 400
Db 384 WKSSDNEEBEVKMKETKQTATVSDLPSTLYCVKQQA--FSEAYNKSSDFSREEC 437
```

RESULT 15

```
Q9PVJ9 CHICK PRELIMINARY; PRT; 442 AA.
AC Q9PVJ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GN Interferon alpha/beta receptor 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR EMBL: AF082667; AAD13679.1; -; Genomic DNA.
DR Ensembl: ENSGALG0000015942; Gallus gallus.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000282; Cytok receptor_2.
DR InterPro: IPR003961; FN_III.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PSS0853; FN3; 4.
KW Receptor.
KW NON TER
FT NON TER
SQ SEQUENCE 442 442 49877 MW; 839EBE92170609E0 CRC64;
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Query Match 31.5%; Score 674.5; DB 2; Length 442;
Best Local Similarity 38.2%; Pred. No. 8.1e-43;
Matches 159; Conservative 76; Mismatches 154; Indels 27; Gaps 12;

Qy 3 NLKSPQKVEVDIIDDNFILAWNRSDSGVNVTFSDYQ----KTGMNDNKLKSGCONIT 57
Db 31 NLKSPQDIQYAVNTFTLWNYTGDT-NVTFSAQYQCFFDLDQTSPEWKELSGCONVS 89
Qy 58 STKCNFSSKLNVYEEIKLRIRAF-KENTISWYEVDSFTPFKAQIGPPEVHLEAEADKAI 116
Db 90 HTECDFSSAITAYDYTHIRAEERREAKSPWISFEMIPYEIAQIGPPEIALQSGINGAI 149
Qy 117 VIHISPTKDSV--MWALDGLSFTYSLIIWKNSSGVEERIENIYSRHKIYKLSPEPTYCL 174
Db 150 KINISPPANQVRKMW-LISVFFKYNVIVDWSNSV-EKVRSLIPDIVINDLAPETTYCL 207
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Qy 175 KVKAAALTSWKIGVSPVHCIKTTVE--NELPPPENIEVSVQNQNYVLKWDYTY--ANMTFQ 232
Db 208 KVQATVPLEDKGLFSPHICIKITRKVNDLLCPTNVRVFPALNMKFYLLWHDNHNHVEHYTYT 267
Qy 233 VQWLHAPLKRNPNGNHLKWKQIPDCENVKTTQC-----VFPQNVFQKGIYLLRVQASDGN 287
Db 268 VQYLTGVLKMLYDDYSKWQKVSVCENITSMKCNLSVVIKPTS----ASYFFRVQAMNEY 323
Qy 288 NTSFMSSEIKFDPTEIOAFLLPPVFNIRSLSDSHIYIGAPKQSGNTPIQDYPILYELIF 347
Db 324 NKSLSKDVEVDPVVTNEIGPPDVKVDISDVLHLHIKITPPGPGNKIMSLDLYDFSYQILY 383
Qy 348 WENTSNAERKIIIEKKTDD--VTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVC 400
Db 384 WKSSDNEEBEVKMKETKQTATVSDLPSTLYCVKQQA--FSEAYNKSSDFSREEC 437
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Search completed: January 17, 2006, 07:18:43  
Job time : 113.108 secs